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JCS710 U.S. PTO

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UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 C.F.R. § 1.53(b))

Attorney Docket No.	MB1-0003
First Inventor or Application Identifier	Heard
Title	Plant Gene Sequences I
Express Mail Label No.	EJ498962678 US

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO: Assistant Commissioner for Patents
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Washington, DC 20231

- ☒ * Fee Transmittal Form (e.g., PTO/SB/17)
(Submit an original and a duplicate for fee processing)
- ☒ Specification [Total Pages **43**]
(preferred arrangement set forth below)
 - Descriptive title of the invention
 - Cross References to Related Applications
 - Statement Regarding Fed sponsored R & D
 - Reference to Microfiche Appendix
 - Background of the invention
 - Brief Summary of the invention
 - Brief Description of the Drawings (if filed)
 - Detailed Description
 - Claim(s)
 - Abstract of the Disclosure
- ☐ Drawing(s) (35 U.S.C. 113) [Total Sheets ☐
- Oath or Declaration [Total Pages - ☒ Newly executed (original or copy)
- ☐ Copy from a prior application (37 C.F.R. § 1.63(d))
(for continuation/divisional with Box 16 completed)
 - ☐ DELETION OF INVENTOR(S)
Signed statement attached deleting inventor(s) named in the prior application, see 37 C.F.R. §§ 1.63(d)(2) and 1.33(b).

- ☐ Microfiche Computer Program (Appendix)
- Nucleotide and/or Amino Acid Sequence Submission (if applicable, all necessary)
 - ☒ Computer Readable Copy
 - ☒ Paper Copy (identical to computer copy)
 - ☒ Statement verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

- ☒ Assignment Papers (cover sheet & document(s))
- ☒ 37 C.F.R. § 3.73(b) Statement (when there is an assignee) ☒ Power of Attorney
- ☐ English Translation Document (if applicable)
- ☐ Information Disclosure Statement (IDS)/PTO-1449 ☐ Copies of IDS Citations
- ☐ Preliminary Amendment
- ☐ Return Receipt Postcard (MPEP 503)
(Should be specifically itemized)
- ☒ * Small Entity Statement(s) ☐ Statement filed in prior application, Status still proper and desired (PTO/SB/09-12)
- ☐ Certified Copy of Priority Document(s) (if foreign priority is claimed)
- ☐ Other:

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17. CORRESPONDENCE ADDRESS

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09/13/99

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application

Inventor(s): Jacqueline Heard et al.

Application No.: Unassigned

Filed: Herewith

Title: Plant Gene Sequences I

VERIFIED STATEMENT CLAIMING SMALL ENTITY STATUS
37 C.F.R. § 1.9(i) AND 1.27(c) - SMALL BUSINESS CONCERN

I hereby declare that I am an official of the small business concern empowered to act on behalf of the concern identified below.

Name: Mendel Biotechnology, Inc.

Address: 21375 Cabot Boulevard, Hayward, California 94545

I hereby declare that the above identified small business concern qualifies as a small business concern as defined in 13 C.F.R. § 121.12, and reproduced in 37 C.F.R. § 1.9(d), for purposes of paying reduced fees under Section 41(a) and (b) of Title 35 U.S.C. in that the number of employees of the concern, including those of its affiliates, does not exceed 500 persons. For purposes of this statement, (1) the number of employees of the business concern is the average over the previous fiscal year of the concern of the persons employed on a full-time, part-time or temporary basis during each of the pay periods of the fiscal year, and (2) concerns are affiliates of each other when either, directly or indirectly, one concern controls or has the power to control the other, or a third-party or parties controls or has the power to control both.

I hereby declare that rights under contract or law have been conveyed to and remain with the small business concern identified above with regard to the invention.

entitled: Plant Gene Sequences I

described in the Specification filed herewith

FILED "OFFICE"

If the rights held by the above-identified small business concern are not exclusive, each individual, concern or organization having rights to the invention is listed below and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 C.F.R. § 1.9(d) or by any concern which would not qualify as a small business concern under 37 C.F.R. § 1.9(d) or a nonprofit organization under 37 C.F.R. § 1.9(e).

NAME:

ADDRESS:

☐ Individual ☐ SmallBusinessConcern ☐ Nonprofit Organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small business entity is no longer appropriate. (37 C.F.R. § 1.28(b)).

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Name of Person Signing: Michael Fromm

Title of Person Signing: President and CEO

Address of Person Signing: 21375 Cabot Boulevard, Hayward, California 94545

Signature: 

Date: 9/8/99

19990908 154600

PLANT GENE SEQUENCES I

The present invention claims priority in part from Provisional Application Serial Nos. 60/101,349, filed September 22, 1998; 60/103,312, filed October 6,
5 1998; 60/108,734, filed November 17, 1998; and 60/113,409, filed December 22, 1998.

FIELD OF THE INVENTION

10 This invention is in the field of plant molecular biology and relates to compositions and methods for modifying a plant's traits.

BACKGROUND OF THE INVENTION

Gene expression levels are controlled in part at the level of transcription, and transcription is affected by transcription factors. Transcription factors regulate
15 gene expression throughout the life cycle of an organism and so are responsible for differential levels of gene expression at various developmental stages, in different tissue and cell types, and in response to different stimuli. Transcription factors may interact with other proteins or with specific sites on a target gene sequence to activate, suppress or otherwise regulate transcription. In addition, the transcription
20 of the transcription factors themselves may be regulated.

Because transcription factors are key controlling elements for biological pathways, altering the expression levels of one or more transcription factors may change entire biological pathways in an organism. For example, manipulation of the levels of selected transcription factors may result in increased expression of
25 economically useful proteins or metabolic chemicals in plants or to improve other agriculturally relevant characteristics. Conversely, blocked or reduced expression of a transcription factor may reduce biosynthesis of unwanted compounds or remove an undesirable trait. Therefore, manipulating transcription factor levels in a plant offers tremendous potential in agricultural biotechnology for modifying a
30 plant's traits.

The present invention provides novel transcription factors for use in modifying a plant's traits

SUMMARY OF THE INVENTION

In one aspect, the present invention relates to an isolated polynucleotide comprising a nucleotide sequence encoding a transcription factor. In one embodiment, the polynucleotide is a sequence provided in the Sequence Listing as

5 SEQ ID No. 1 (G4), SEQ ID No. 3 (G5), SEQ ID No. 5 (G8), SEQ ID No. 7 (G9), SEQ ID No. 9 (G10), SEQ ID No. 11 (G14), SEQ ID No. 13 (G864), SEQ ID No. 15 (G865), SEQ ID No. 17 (G867), SEQ ID No. 19 (G869), SEQ ID No. 21 (G872), SEQ ID No. 23 (G971), SEQ ID No. 25 (G974), SEQ ID No. 27 (G975), SEQ ID No. 29 (G976), SEQ ID No. 31 (G977), SEQ ID No. 33 (G979), SEQ ID

10 No. 35 (G993), SEQ ID No. 37 (G1020), SEQ ID No. 39 (G1023), SEQ ID No. 41 (G661), SEQ ID No. 43 (G663), SEQ ID No. 45 (G664), SEQ ID No. 47 (G672), SEQ ID No. 49 (G673), SEQ ID No. 51 (G675), SEQ ID No. 53 (G677), SEQ ID No. 55 (G679), SEQ ID No. 57 (G932), SEQ ID No. 59 (G994), SEQ ID No. 61 (G996), SEQ ID No. 63 (G997), SEQ ID No. 65 (G1328), SEQ ID No. 67 (G858),

15 SEQ ID No. 69 (G860), SEQ ID No. 71 (G861), SEQ ID No. 73 (G866), SEQ ID No. 75 (G877), SEQ ID No. 77 (G878), SEQ ID No. 79 (G883), SEQ ID No. 81 (G884), SEQ ID No. 83 (G920), SEQ ID No. 85 (G921), SEQ ID No. 87 (G986), SEQ ID No. 89 (G1022), SEQ ID No. 91 (G1043), SEQ ID No. 93 (G1091), SEQ ID No. 95 (G837), SEQ ID No. 97 (G838), SEQ ID No. 99 (G850), SEQ ID No.

20 101 (G1241), SEQ ID No. 103 (G749), SEQ ID No. 105 (G751), SEQ ID No. 107 (G897), SEQ ID No. 109 (G902), SEQ ID No. 111 (G905), SEQ ID No. 113 (G908), SEQ ID No. 115 (G909), SEQ ID No. 117 (G911), SEQ ID No. 119 (G1255), SEQ ID No. 121 (G1258), SEQ ID No. 123 (G399), SEQ ID No. 125 (G699), SEQ ID No. 127 (G964), SEQ ID No. 129 (G1334), SEQ ID No. 131 (G718), SEQ ID No. 133 (G763), SEQ ID No. 135 (G462), SEQ ID No. 137 (G782), SEQ ID No. 139 (G783), SEQ ID No. 141 (G786), SEQ ID No. 143 (G793), SEQ ID No. 145 (G801), SEQ ID No. 147 (G802), SEQ ID No. 149 (G1065), SEQ ID No. 151 (G629), SEQ ID No. 153 (G630), SEQ ID No. 155 (G735), SEQ ID No. 157 (G1034), SEQ ID No. 159 (G1035), SEQ ID No. 161 (G1048), SEQ ID No. 163 (G1058), SEQ ID No. 165 (G849), SEQ ID No. 167 (G726), or SEQ ID No. 169 (G1197).

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In another embodiment, the polynucleotide of the invention is one that is homologous to a polynucleotide provided in the Sequence Listing as determined under stringent hybridization conditions or by the analysis of sequence identity

criteria. In yet another embodiment, the polynucleotide may comprise a sequence comprising a fragment of at least 15 consecutive nucleotides of a polynucleotide sequence of the invention. The polynucleotide may further comprise a promoter operably linked to the sequence. The promoter may be a constitutive, an inducible or a tissue-active promoter.

In a second aspect, the present invention relates to an isolated polypeptide that is a transcription factor. In one embodiment, the polypeptide comprises a sequence provided in the Sequence Listing as SEQ ID No. 2 (G4 prot), SEQ ID No. 4 (G5 prot), SEQ ID No. 6 (G8 prot), SEQ ID No. 8 (G9 prot), SEQ ID No. 10 (G10 prot), SEQ ID No. 12 (G14 prot), SEQ ID No. 14 (G864 prot), SEQ ID No. 16 (G865 prot), SEQ ID No. 18 (G867 prot), SEQ ID No. 20 (G869 prot), SEQ ID No. 22 (G872 prot), SEQ ID No. 24 (G971 prot), SEQ ID No. 26 (G974 prot), SEQ ID No. 28 (G975 prot), SEQ ID No. 30 (G976 prot), SEQ ID No. 32 (G977 prot), SEQ ID No. 34 (G979 prot), SEQ ID No. 36 (G993 prot), SEQ ID No. 38 (G1020 prot), SEQ ID No. 40 (G1023 prot), SEQ ID No. 42 (G661 prot), SEQ ID No. 44 (G663 prot), SEQ ID No. 46 (G664 prot), SEQ ID No. 48 (G672 prot), SEQ ID No. 50 (G673 prot), SEQ ID No. 52 (G675 prot), SEQ ID No. 54 (G677 prot), SEQ ID No. 56 (G679 prot), SEQ ID No. 58 (G932 prot), SEQ ID No. 60 (G994 prot), SEQ ID No. 62 (G996 prot), SEQ ID No. 64 (G997 prot), SEQ ID No. 66 (G1328 prot), SEQ ID No. 68 (G858 prot), SEQ ID No. 70 (G860 prot), SEQ ID No. 72 (G861 prot), SEQ ID No. 74 (G866 prot), SEQ ID No. 76 (G877 prot), SEQ ID No. 78 (G878 prot), SEQ ID No. 80 (G883 prot), SEQ ID No. 82 (G884 prot), SEQ ID No. 84 (G920 prot), SEQ ID No. 86 (G921 prot), SEQ ID No. 88 (G986 prot), SEQ ID No. 90 (G1022 prot), SEQ ID No. 92 (G1043 prot), SEQ ID No. 94 (G1091 prot), SEQ ID No. 96 (G837 prot), SEQ ID No. 98 (G838 prot), SEQ ID No. 100 (G850 prot), SEQ ID No. 102 (G1241), SEQ ID No. 104 (G749 prot), SEQ ID No. 106 (G751 prot), SEQ ID No. 108 (G897 prot), SEQ ID No. 110 (G902 prot), SEQ ID No. 112 (G905 prot), SEQ ID No. 114 (G908 prot), SEQ ID No. 116 (G909 prot), SEQ ID No. 118 (G911 prot), SEQ ID No. 120 (G1255 prot), SEQ ID No. 122 (G1258 prot), SEQ ID No. 124 (G399 prot), SEQ ID No. 126 (G699 prot), SEQ ID No. 128 (G964 prot), SEQ ID No. 130 (G1334 prot), SEQ ID No. 132 (G718 prot), SEQ ID No. 134 (G763 prot), SEQ ID No. 136 (G462 prot), SEQ ID No. 138 (G782 prot), SEQ ID No. 140 (G783 prot), SEQ ID No. 142 (G786 prot), SEQ ID No. 144 (G793 prot), SEQ ID No. 146 (G801

prot), SEQ ID No. 148 (G802 prot), SEQ ID No. 150 (G1065 prot), SEQ ID No. 152 (G629 prot), SEQ ID No. 154 (G630 prot), SEQ ID No. 156 (G735 prot), SEQ ID No. 158 (G1034 prot), SEQ ID No. 160 (G1035 prot), SEQ ID No. 162 (G1048 prot), SEQ ID No. 164 (G1058 prot), SEQ ID No. 166 (G849 prot), SEQ ID No. 168 (G726 prot), or SEQ ID No. 170 (G1197 prot).

In another embodiment, the polypeptide comprises a sequence with one or more substitutions, deletions or insertions to a sequence provided in the Sequence Listing or a sequence which when ectopically expressed in a plant modifies a plant trait in a similar manner as a sequence provided in the Sequence Listing. The polypeptide may also comprise a fragment of at least 6 consecutive amino acids of a sequence provided in the Sequence Listing.

The invention also comprises an expression vector comprising a polynucleotide described above, a host cell comprising the expression vector or a transgenic plant comprising an isolated polynucleotide or polypeptide described above.

The invention also provides a method for producing a transgenic plant comprising an isolated polynucleotide or polypeptide described above. The method comprises (a) ectopically expressing an isolated polynucleotide encoding a polypeptide of the invention in a plant; and (b) selecting a plant expressing the polynucleotide.

In another aspect the invention provides a method for screening for one or more molecules to identify a molecule that modifies the expression of a polynucleotide or polypeptide of the invention in a plant. The method entails (a) placing the molecule in contact with the plant; and (b) monitoring the effect of the molecule on the expression of the polynucleotide or polypeptide in the plant.

In yet another aspect, the invention provides a method for identifying a sequence homologous to a polynucleotide or polypeptide sequence provided in the Sequence Listing. The method comprises (a) providing a database sequence; (b) aligning and comparing the sequence provided with the database sequence to determine whether the database sequence meets sequence identity criteria relative to the sequence provided herein; and (c) selecting any database sequence that meets the sequence identity criteria. The present invention also encompasses a homologous polypeptide or polynucleotide identified by the method and a transgenic plant comprising the homologous sequence.

The invention further provides a method for screening for a transcription factor that modifies a plant trait, said method comprising (a) generating one or more transgenic plants ectopically expressing an isolated polynucleotide of claim 1 and (b) identifying from said generated transgenic plants a plant with a modified plant trait.

DETAILED DESCRIPTION OF THE INVENTION

DEFINITIONS

A “polynucleotide” is a nucleotide sequence comprising a gene coding sequence or a fragment thereof (comprising at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides, and more preferably at least 50 consecutive nucleotides), a promoter, an intron, an enhancer region, a polyadenylation site, a translation initiation site, 5’ or 3’ untranslated regions, a reporter gene, a selectable marker or the like. The polynucleotide may comprise single stranded or double stranded DNA or RNA. The polynucleotide may comprise modified bases or a modified backbone. The polynucleotide may be genomic, a transcript (such as an mRNA) or a processed nucleotide sequence (such as a cDNA). The polynucleotide may comprise a sequence in either sense or antisense orientations.

An “isolated polynucleotide” is a polynucleotide that is not in its native state, e.g., the polynucleotide is comprised of a nucleotide sequence not found in nature or the polynucleotide is separated from nucleotide sequences with which it typically is in proximity or is next to nucleotide sequences with which it typically is not in proximity.

An “isolated polypeptide” is a polypeptide derived from the translation of an isolated polynucleotide or is more enriched in a cell than the polypeptide in its natural state in a wild type cell, e.g. more than 5% enriched, more than 10% enriched or more than 20% enriched and is not the result of a natural response of a wild type plant or is separated from other components with which it is typically associated with in a cell.

A “transgenic plant” refers to a plant that contains genetic material not normally found in a wild type plant of the same species, or in a naturally occurring variety or in a cultivar, and which has been introduced into the plant by human

manipulation. A transgenic plant is a plant that may contain an expression vector or cassette. The expression cassette comprises a gene coding sequence and allows for the expression of the gene coding sequence. The expression cassette may be introduced into a plant by transformation or by breeding after transformation of a parent plant.

The transgenic plant may comprise machinery, such as the T-DNA activation tagging machinery, necessary for ectopically expressing an endogenous gene coding sequence. T-DNA activation tagging entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has been inserted in the genome, expression of a flanking gene coding sequence becomes deregulated (Ichikawa et al., (1997) *Nature* 390: 698-701; Kakimoto et al., *Science* 274: 982-985 (1996)). The transgenic plant may also comprise the machinery necessary for expressing or altering the activity of a polypeptide encoded by an endogenous gene, for example by altering the phosphorylation state of the polypeptide to maintain it in an activated state. A transgenic plant refers to a whole plant as well as to a plant part, such as seed, fruit, leave, or root, plant tissue, plant cells or any other plant material, and progeny thereof.

The phrase “ectopically expressed” in reference to polynucleotide or polypeptide expression refers to an expression pattern in the transgenic plant that is different from the expression pattern in the wild type plant or a reference; for example, by expression in a cell type other than a cell type in which the sequence is expressed in the wild type plant, or by expression at a time other than at the time the sequence is expressed in the wild type plant, or by a response to different inducible agents, such as hormones or environmental signals, or at different expression levels (either higher or lower) compared with those found in a wild type plant. The term also refers to lowering the levels of expression to below the detection level or completely abolishing expression. The resulting expression pattern may be transient or stable.

A “transcription factor” (TF) refers to a polypeptide that controls the expression of a gene or genes either directly by binding to one or more nucleotide sequences associated with a gene coding sequence or indirectly by affecting the level or activity of other polypeptides that do bind directly to one or more nucleotide sequences associated with a gene coding sequence. A transcription factor may activate or repress expression of a gene or genes.

The transcription factor sequence may comprise a whole coding sequence or a fragment or domain of a coding sequence. A “fragment or domain”, as referred to polypeptides, may be a portion of a polypeptide which performs at least one biological function of the intact polypeptide in substantially the same manner or to a similar extent as does the intact polypeptide, e.g. those fragments provided in Table 1. A fragment may comprise, for example, a DNA binding domain that binds to a specific DNA binding region, an activation domain or a domain for protein-protein interactions. Fragments may vary in size from as few as 6 amino acids to the length of the intact polypeptide, but are preferably at least 30 amino acids in length and more preferably 60 amino acids in length. In reference to a nucleotide sequence “a fragment” refers to any sequence of at least consecutive 15 nucleotides, preferably at least 30 nucleotides, more preferably at least 50, of any of the sequences provided herein and as an example include nucleotides 1-100, 101-200, 201-300, 501-600, 801-900, 1000-1015, or 1101-1300 of SEQ ID No. 1.

“Trait” refers to a physiological, morphological, biochemical or physical characteristic of a plant or particular plant material or cell. This characteristic may be visible to the human eye, such as seed or plant size, or be measured by biochemical techniques, such as the protein, starch or oil content of seed or leaves or by the observation of the expression level of genes by employing Northernblots, RT PCR, microarray gene expression assays or reporter gene expression systems or be measured by agricultural observations such as stress tolerance, yield or disease resistance.

“Trait modification” refers to a detectable difference in a characteristic in a transgenic plant ectopically expressing a polynucleotide or polypeptide of the present invention relative to a plant not doing so, such as a wild type plant. The trait modification may entail at least a 5% increase or decrease in an observed trait (difference), at least a 10% difference, at least a 20% difference, at least a 30%, at least a 50%, at least a 70%, at least a 100% or a greater difference. It is known that there may be a natural variation in the modified trait. Therefore, the trait modification observed entails a change of the normal distribution of the trait in transgenic plants compared with the distribution observed in wild type plant.

Trait modifications of particular interest include those to seed (embryo), fruit, root, flower, leaf, stem, shoot, seedling or the like, including: enhanced tolerance to environmental conditions including freezing, chilling, heat, drought,

water saturation, radiation and ozone; enhanced resistance to microbial, fungal or viral diseases; decreased herbicide sensitivity, enhanced tolerance of heavy metals (or enhanced ability to take up heavy metals), enhanced growth under poor photoconditions (e.g., low light and/or short day length), or changes in expression levels of genes of interest. Other phenotype that may be modified relate to the production of plant metabolites, such as variations in the production of taxol, tocopherol, tocotrienol, sterols, phytosterols, vitamins, wax monomers, antioxidants, amino acids, lignins, cellulose, tannins, prenyllipids (such as chlorophylls and carotenoids), glucosinolates, and terpenoids, enhanced or compositionally altered protein or oil production (especially in seeds), or modified sugar (insoluble or soluble) and/or starch composition. Physical plant characteristics that may be modified include cell development (such as the number of trichomes), fruit and seed size and number, yields of plant parts such as stems, leaves and roots, the stability of the seeds during storage, characteristics of the seed pod (e.g., susceptibility to shattering), root hair length and quantity, internode distances, or the quality of seed coat. Plant growth characteristics that may be modified include growth rate, germination rate of seeds, vigor of plants and seedlings, leaf and flower senescence, male sterility, apomixis, flowering time, flower abscission, rate of nitrogen uptake, biomass or transpiration characteristics, as well as plant architecture characteristics such as apical dominance, branching patterns, number of organs, organ identity, organ shape or size.

1. The Sequences

We have discovered novel polynucleotides and polypeptides that are plant transcription factors. The plant transcription factors are derived from *Arabidopsis thaliana* and belong to one of the following transcription factor families: the AP2 (APETALA2) domain transcription factor family (Riechmann and Meyerowitz (1998) *J. Biol. Chem.* 379:633-646); the MYB transcription factor family (Martin and Paz-Ares, (1997) *Trends Genet.* 13:67-73); the MADS domain transcription factor family (Riechmann and Meyerowitz (1997) *J. Biol. Chem.* 378:1079-1101); the WRKY protein family (Ishiguro and Nakamura (1994) *Mol. Gen. Genet.* 244:563-571); the ankyrin-repeat protein family (Zhang et al. (1992) *Plant Cell* 4:1575-1588); the miscellaneous protein (MISC) family (Kim et al. (1997) *Plant J.* 11:1237-1251); the zinc finger protein (Z) family (Klug and Schwabe (1995)

FASEB J. 9: 597-604); the homeobox (HB) protein family (Duboule (1994) *Guidebook to the Homeobox Genes*, Oxford University Press); the CAAT-element binding proteins (Forsburg and Guarente (1989) *Genes Dev.* 3:1166-1178); the squamosa promoter binding proteins (SPB) (Klein et al. (1996) *Mol. Gen. Genet.* 1996 250:7-16); the NAM protein family; the IAA/AUX proteins (Rouse et al. (1998) *Science* 279:1371-1373); the HLH/MYC protein family (Littlewood et al. (1994) *Prot. Profile* 1:639-709); the DNA-binding protein (DBP) family (Tucker et al. (1994) *EMBO J.* 13:2994-3002); the bZIP family of transcription factors (Foster et al. (1994) *FASEB J.* 8:192-200); the BPF-1 protein (Box P-binding factor) family (da Costa e Silva et al. (1993) *Plant J.* 4:125-135); and the golden protein (GLD) family (Hall et al. (1998) *Plant Cell* 10:925-936

The novel polynucleotides and polypeptides are provided in the Sequence Listing and are tabulated in Table 1. Table 1 identifies a SEQ ID No., its corresponding GID number, the transcription factor family to which the sequence belongs, fragments derived from the sequences and whether the sequence is a polynucleotide or a polypeptide sequence. Producing transgenic plants with modified expression levels of one or more of these transcription factors compared with those levels found in a wild type plant may be used to modify a plant's traits. The effect of modifying the expression levels of a particular transcription factor on the traits of a transgenic plant is described further in the Examples.

We have also identified domains or fragments derived from the sequences. The numbers indicating the fragment location for the cDNA sequences may be from either 5' or 3' end of the cDNA. For the protein sequences the fragment location is determined from the N-terminus of the protein and may include adjacent amino acid sequences, such as for example for SEQ ID No. 2 an additional 10, 20, 40, 60 or 100 amino acids in either N-terminal or C-terminal direction of the polypeptide.

Table 1

SEQ ID No.	GID No. (Family)	Fragments	CDNA or protein
1	G4 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	CDNA
2	G4 (AP2)	121-188	Protein
3	G5 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	CDNA
4	G5 (AP2)	149-216	Protein
5	G8 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	CDNA
6	G8 (AP2)	151-0217 and 243-295	Protein
7	G9 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	CDNA
8	G9 (AP2)	62-127	protein
9	G10 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
10	G10 (AP2)	21-88	protein
11	G14 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
12	G14 (AP2)	122-189	protein
13	G864 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
14	G864 (AP2)	119-186	protein
15	G865 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
16	G865 (AP2)	36-103	protein
17	G867 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
18	G867 (AP2)	59-124	protein
19	G869 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
20	G869 (AP2)	110-177	protein
21	G872 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
22	G872 (AP2)	18-85	protein
23	G971 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
24	G971 (AP2)	120-186	protein
25	G974 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
26	G974 (AP2)	80-147	protein
27	G975 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
28	G975 (AP2)	4-71	protein
29	G976 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
30	G976 (AP2)	86-153	protein
31	G977 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
32	G977 (AP2)	5-72	protein
33	G979 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
34	G979 (AP2)	63-139 and 165-233	protein
35	G993 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
36	G993 (AP2)	69-134	protein
37	G1020 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
38	G1020 (AP2)	28-95	protein
39	G1023 (AP2)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
40	G1023 (AP2)	128-195	protein
41	G661 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
42	G661 (MYB)	12-117	protein
43	G663 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
44	G663 (MYB)	8-112	protein
45	G664 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
46	G664 (MYB)	12-116	protein
47	G672 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
48	G672 (MYB)	90-160	protein
49	G673 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
50	G673 (MYB)	36-123	protein
51	G675 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
52	G675 (MYB)	12-126	protein

53	G677 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
54	G677 (MYB)	12-116	protein
55	G679 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
56	G679 (MYB)	98-166	protein
57	G932 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
58	G932 (MYB)	12-112	protein
59	G994 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
60	G994 (MYB)	13-111	protein
61	G996 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
62	G996 (MYB)	12-104	protein
63	G997 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
64	G997 (MYB)	11-36	protein
65	G1328 (MYB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
66	G1328 (MYB)	13-114	protein
67	G858 (MADS)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
68	G858 (MADS)	2-57	protein
69	G860 (MADS)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
70	G860 (MADS)	2-57	protein
71	G861 (MADS)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
72	G861 (MADS)	2-57	protein
73	G866 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
74	G866 (WRKY)	243-300	protein
75	G877 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
76	G877 (WRKY)	273-328 and 487-543	protein
77	G878 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
78	G878 (WRKY)	250-305 and 415-471	protein
79	G883 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
80	G883 (WRKY)	249-306	protein
81	G884 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
82	G884 (WRKY)	229-284 and 409-465	protein
83	G920 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
84	G920 (WRKY)	152-211	protein
85	G921 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
86	G921 (WRKY)	146-203	protein
87	G986 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
88	G986 (WRKY)	146-203	protein
89	G1022 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
90	G1022 (WRKY)	281-338	protein
91	G1043 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
92	G1043 (WRKY)	119-179	protein
93	G1091 (WRKY)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
94	G1091 (WRKY)	262-319	protein
95	G837 (AKR)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
96	G837 (AKR)	362-412	protein
97	G838 (AKR)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
98	G838 (AKR)	279-321	protein
99	G850 (MISC)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
100	G850 (MISC)	491-517	protein
101	G1241 (MISC)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
102	G1241 (MISC)	-----	protein
103	G749 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
104	G749 (Z)	125-143	protein
105	G751 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
106	G751 (Z)	37-82	protein
107	G897 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
108	G897 (Z)	8-90	protein
109	G902 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
110	G902 (Z)	56-91	protein

111	G905 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
112	G905 (Z)	118-160	protein
113	G908 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
114	G908 (Z)	8-29and 72-88	protein
115	G909 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
116	G909 (Z)	17-68	protein
117	G911 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
118	G911 (Z)	86-129	protein
119	G1255 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
120	G1255 (Z)	17-54	protein
121	G1258 (Z)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
122	G1258 (Z)	57-108	protein
123	G399 (HB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
124	G399 (HB)	160-181	protein
125	G699 (HB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
126	G699 (HB)	89-108	protein
127	G964 (HB)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
128	G964 (HB)	160-179	protein
129	G1334 (CAAT)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
130	G1334 (CAAT)	137-188	protein
131	G718 (SPBP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
132	G718 (SPBP)	176-244	protein
133	G763 (NAM)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
134	G763 (NAM)	14-160	protein
135	G462 (IAA/AUX)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
136	G462 (IAA/AUX)	11-20, 67-82, 98-131, 152-181	protein
137	G782 (HLH/MYC)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
138	G782 (HLH/MYC)	9-28	protein
139	G783 (HLH/MYC)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
140	G783 (HLH/MYC)	31-46	protein
141	G786 (HLH/MYC)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
142	G786 (HLH/MYC)	220-242	protein
143	G793 (HLH/MYC)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
144	G793 (HLH/MYC)	182-206	protein
145	G801 (DBP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
146	G801 (DBP)	51-68	protein
147	G802 (DBP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
148	G802 (DBP)	80-97	protein
149	G1065 (DBP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
150	G1065 (DBP)	146-167	protein
151	G629 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
152	G629 (bZIP)	100-125	protein
153	G630 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
154	G630 (bZIP)	80-105	protein
155	G735 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
156	G735 (bZIP)	160-185	protein
157	G1034 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
158	G1034 (bZIP)	109-134	protein
159	G1035 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
160	G1035 (bZIP)	47-72	protein
161	G1048 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
162	G1048 (bZIP)	150-175	protein
163	G1058 (bZIP)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
164	G1058 (bZIP)	299-324	protein
165	G849 (BPF)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
166	G849 (BPF)	509-583	protein
167	G726 (GLD)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
168	G726 (GLD)	20-69	protein

169	G1197 (GLD)	1-100, 30-45, 75-125, 150-200, 200-300, 350-400	cDNA
170	G1197 (GLD)	42-90	protein

The identified polypeptide fragments may be combined with fragments or sequences derived from other transcription factors so as to generate additional novel sequences, such as by employing the methods described in Short, PCT publication WO9827230, entitled "Methods and Compositions for Polypeptide Engineering" or in Patten et al., PCT publication WO9923236, entitled "Method of DNA Shuffling".

The identified polynucleotide fragments are useful as nucleic acid probes and primers. A nucleic acid probe is useful in hybridization protocols, including protocols for microarray experiments. Primers may be annealed to a complementary target DNA strand by nucleic acid hybridization to form a hybrid between the primer and the target DNA strand, and then extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR) or other nucleic-acid amplification methods. See Sambrook et al., *Molecular Cloning. A Laboratory Manual*, Ed. 2, Cold Spring Harbor Laboratory Press, New York (1989) and Ausubel et al. (eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1998).

2. Identification of Homologous Sequences (Homologs)

Homologous sequences to those provided in the Sequence Listing derived from *Arabidopsis thaliana* or from other plants may be used to modify a plant trait. Homologous sequences may be derived from any plant including monocots and dicots and in particular agriculturally important plant species, including but not limited to, crops such as soybean, wheat, corn, potato, cotton, rice, oilseed rape (including canola), sunflower, alfalfa, sugarcane and turf; or fruits and vegetables, such as banana, blackberry, blueberry, strawberry, and raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honeydew, lettuce, mango, melon, onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits (such as apple, peach, pear, cherry and plum) and vegetable brassicas (such as broccoli, cabbage, cauliflower, brussel sprouts and kohlrabi). Other crops, fruits and vegetables whose phenotype may be changed include barley, currant, avocado, citrus fruits such as oranges, lemons,

grapefruit and tangerines, artichoke, cherries, nuts such as the walnut and peanut, endive, leek, roots, such as arrowroot, beet, cassava, turnip, radish, yam, sweet potato and beans. The homologs may also be derived from woody species, such pine, poplar and eucalyptus.

5 Substitutions, deletions and insertions introduced into the sequences provided in the Sequence Listing are also envisioned by the invention. Such sequence modifications can be engineered into a sequence by site-directed mutagenesis (Wu (ed.) *Meth. Enzymol.* (1993) vol. 217, Academic Press). Amino acid substitutions are typically of single residues; insertions usually will be on the order of about from 1 to 10 amino acid residues; and deletions will range about from 1 to 30 residues. In preferred embodiments, deletions or insertions are made in adjacent pairs, e.g., a deletion of two residues or insertion of two residues. Substitutions, deletions, insertions or any combination thereof may be combined to arrive at a sequence. The mutations that are made in the polynucleotide encoding the transcription factor should not place the sequence out of reading frame and should not create complementary regions that could produce secondary mRNA structure. Preferably, the polypeptide encoded by the DNA should perform the desired function.

15 Substitutions are those in which at least one residue in the amino acid sequence has been removed and a different residue inserted in its place. Such substitutions generally are made in accordance with the following Table 2 when it is desired to maintain the activity of the protein. Table 2 shows amino acids which may be substituted for an amino acid in a protein and which are typically regarded as conservative substitutions.

Table 2	
Residue	Conservative Substitutions
Ala	Ser
Arg	Lys
Asn	Gln; His
Asp	Glu
Gln	Asn
Cys	Ser
Glu	Asp
Gly	Pro
His	Asn; Gln
Ile	Leu, Val
Leu	Ile; Val
Lys	Arg; Gln
Met	Leu; Ile
Phe	Met; Leu; Tyr
Ser	Thr; Gly
Thr	Ser; Val
Trp	Tyr
Tyr	Trp; Phe
Val	Ile; Leu

Substitutions that are less conservative than those in Table 2 may be selected by picking residues that differ more significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in protein properties will be those in which (a) a hydrophilic residue, e.g., seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g., leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g., lysyl, arginyl,

or histidyl, is substituted for (or by) an electronegative residue, e.g., glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine.

Additionally, the term “homologous sequence” encompasses a polypeptide sequence that is modified by chemical or enzymatic means. The homologous sequence may be a sequence modified by lipids, sugars, peptides, organic or inorganic compounds, by the use of modified amino acids or the like. Protein modification techniques are illustrated in Ausubel et al. (eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1998).

Homologous sequences also means two sequences having a substantial percentage of sequence identity after alignment as determined by using sequence analysis programs for database searching and sequence alignment and comparison available, for example, from the Wisconsin Package Version 10.0, such as BLAST, FASTA, PILEUP, FINDPATTERNS or the like (GCG, Madison, WI). Public sequence databases such as GenBank, EMBL, Swiss-Prot and PIR or private sequence databases such as PhytoSeq (Incyte Pharmaceuticals, Palo Alto, CA) may be searched. Alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981) *Adv. Appl. Math.* 2:482, by the homology alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity method of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. U.S.A.* 85: 2444, by computerized implementations of these algorithms. After alignment, sequence comparisons between two (or more) polynucleotides or polypeptides are typically performed by comparing sequences of the two sequences over a comparison window to identify and compare local regions of sequence similarity. The comparison window may be a segment of at least about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 contiguous positions. A description of the method is provided in Ausubel et al. (eds) (1999) *Current Protocols in Molecular Biology*, John Wiley & Sons.

Transcription factors that are homologs of the disclosed sequences will typically share at least 40% amino acid sequence identity. More closely related TFs may share at least 50%, 60%, 65%, 70%, 75% or 80% sequence identity with the disclosed sequences. Factors that are most closely related to the disclosed sequences share at least 85%, 90% or 95% sequence identity. At the nucleotide

level, the sequences will typically share at least 40% nucleotide sequence identity, preferably at least 50%, 60%, 70% or 80% sequence identity, and more preferably 85%, 90%, 95% or 97% sequence identity. The degeneracy of the genetic code enables major variations in the nucleotide sequence of a polynucleotide while maintaining the amino acid sequence of the encoded protein.

One way to identify whether two nucleic acid molecules are closely related is that the two molecules hybridize to each other under stringent conditions. Generally, stringent conditions are selected to be about 5°C to 20°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. Conditions for nucleic acid hybridization and calculation of stringencies can be found in Sambrook et al. (1989) *Molecular Cloning. A Laboratory Manual*, Ed. 2, Cold Spring Harbor Laboratory Press, New York and Tijssen (1993) *Laboratory Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Acid Probes* Part I, Elsevier, New York. Nucleic acid molecules that hybridize under stringent conditions will typically hybridize to a probe based on either the entire cDNA or selected portions of the cDNA under wash conditions of 0.2x SSC to 2.0 x SSC, 0.1% SDS at 50-65° C, for example 0.2 x SSC, 0.1% SDS at 65° C. For detecting less closely related homologs washes may be performed at 50° C.

For conventional hybridization the hybridization probe is conjugated with a detectable label such as a radioactive label, and the probe is preferably of at least 20 nucleotides in length. As is well known in the art, increasing the length of hybridization probes tends to give enhanced specificity. The labeled probe derived from the *Arabidopsis* nucleotide sequence may be hybridized to a plant cDNA or genomic library and the hybridization signal detected using means known in the art. The hybridizing colony or plaque (depending on the type of library used) is then purified and the cloned sequence contained in that colony or plaque isolated and characterized. Homologs may also be identified by PCR-based techniques, such as inverse PCR or RACE, using degenerate primers. See Ausubel et al. (eds) (1998) *Current Protocols in Molecular Biology*, John Wiley & Sons.

TF homologs may alternatively be obtained by immunoscreening an expression library. With the provision herein of the disclosed TF nucleic acid

sequences, the polypeptide may be expressed and purified in a heterologous expression system (e.g., *E. coli*) and used to raise antibodies (monoclonal or polyclonal) specific for the TF. Antibodies may also be raised against synthetic peptides derived from TF amino acid sequences. Methods of raising antibodies are well known in the art and are described in Harlow and Lane (1988) *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York. Such antibodies can then be used to screen an expression library produced from the plant from which it is desired to clone the TF homolog, using the methods described above. The selected cDNAs may be confirmed by sequencing and enzymatic activity.

3. Ectopic Expression of Transcription Factors

Any of the identified sequences may be incorporated into a cassette or vector for expression in plants. A number of expression vectors suitable for stable transformation of plant cells or for the establishment of transgenic plants have been described including those described in Weissbach and Weissbach, (1989) *Methods for Plant Molecular Biology*, Academic Press, and Gelvin et al., (1990) *Plant Molecular Biology Manual*, Kluwer Academic Publishers. Specific examples include those derived from a Ti plasmid of *Agrobacterium tumefaciens*, as well as those disclosed by Herrera-Estrella, L., et al., (1983) *Nature* 303: 209, Bevan, M., *Nucl. Acids Res.* (1984) 12: 8711-8721, Klee, H. J., (1985) *Bio/Technology* 3: 637-642, for dicotyledonous plants.

Alternatively, non-Ti vectors can be used to transfer the DNA into monocotyledonous plants and cells by using free DNA delivery techniques. Such methods may involve, for example, the use of liposomes, electroporation, microprojectile bombardment, silicon carbide whiskers, and viruses. By using these methods transgenic plants such as wheat, rice (Christou, P., (1991) *Bio/Technology* 9: 957-962) and corn (Gordon-Kamm, W., (1990) *Plant Cell* 2: 603-618) can be produced. An immature embryo can also be a good target tissue for monocots for direct DNA delivery techniques by using the particle gun (Weeks, T. et al., (1993) *Plant Physiol.* 102: 1077-1084; Vasil, V., (1993) *Bio/Technology* 10: 667-674; Wan, Y. and Lemeaux, P., (1994) *Plant Physiol.* 104: 37-48, and for *Agrobacterium*-mediated DNA transfer (Ishida et al., (1996) *Nature Biotech.* 14: 745-750).

Typically, plant transformation vectors include one or more cloned plant coding sequence (genomic or cDNA) under the transcriptional control of 5' and 3' regulatory sequences and a dominant selectable marker. Such plant transformation vectors typically also contain a promoter (e.g., a regulatory region controlling inducible or constitutive, environmentally-or developmentally-regulated, or cell- or tissue-specific expression), a transcription initiation start site, an RNA processing signal (such as intron splice sites), a transcription termination site, and/or a polyadenylation signal.

Examples of constitutive plant promoters which may be useful for expressing the TF sequence include: the cauliflower mosaic virus (CaMV) 35S promoter, which confers constitutive, high-level expression in most plant tissues (see, e.g., Odel et al., (1985) *Nature* 313:810); the nopaline synthase promoter (An et al., (1988) *Plant Physiol.* 88:547); and the octopine synthase promoter (Fromm et al., (1989) *Plant Cell* 1: 977).

A variety of plant gene promoters that regulate gene expression in response to environmental, hormonal, chemical, developmental signals, and in a tissue-active manner can be used for expression of the TF sequence in plants, as illustrated seed-specific promoters (such as the napin, phaseolin or DC3 promoter described in US Pat. No. 5,773,697), fruit-specific promoters that are active during fruit ripening (such as the dru 1 promoter (US Pat. No. 5,783,393), or the 2A11 promoter (US Pat. No. 4,943,674) and the tomato polygalacturonase promoter (Bird et al. (1988) *Plant Mol. Biol.* 11:651), root-specific promoters, such as those disclosed in US Patent Nos. 5,618,988, 5,837,848 and 5,905,186, pollen-active promoters such as PTA29, PTA26 and PTA13 (US Pat. No. 5,792,929), promoters active in vascular tissue (Ringli and Keller (1998) *Plant Mol. Biol.* 37:977-988), flower-specific (Kaiser et al, (1995) *Plant Mol. Biol.* 28:231-243), pollen (Baerson et al. (1994) *Plant Mol. Biol.* 26:1947-1959), carpels (Ohl et al. (1990) *Plant Cell* 2:837-848), pollen and ovules (Baerson et al. (1993) *Plant Mol. Biol.* 22:255-267), auxin-inducible promoters (such as that described in van der Kop et al (1999) *Plant Mol. Biol.* 39:979-990 or Baumann et al. (1999) *Plant Cell* 11:323-334), cytokinin-inducible promoter (Guevara-Garcia (1998) *Plant Mol. Biol.* 38:743-753), promoters responsive to gibberellin (Shi et al. (1998) *Plant Mol. Biol.* 38:1053-1060, Willmott et al. (1998) 38:817-825) and the like. Additional promoters are those that elicit expression in response to heat (Ainley, et al. (1993) *Plant Mol. Biol.*

22: 13-23), light (*e.g.*, the pea *rbcS*-3A promoter, Kuhlemeier et al., (1989) *Plant Cell* 1:471, and the maize *rbcS* promoter, Schaffner and Sheen, (1991) *Plant Cell* 3: 997); wounding (*e.g.*, *wun1*, Siebertz et al., (1989) *Plant Cell* 1: 961); pathogen resistance, and chemicals such as methyl jasmonate or salicylic acid (Gatz et al., (1997) *Plant Mol. Biol.* 48: 89-108). In addition, the timing of the expression can be controlled by using promoters such as those acting at senescence (An and Amazon (1995) *Science* 270: 1986-1988); or late seed development (Odell et al. (1994) *Plant Physiol.* 106:447-458).

Plant expression vectors may also include RNA processing signals that may be positioned within, upstream or downstream of the coding sequence. In addition, the expression vectors may include additional regulatory sequences from the 3'-untranslated region of plant genes, *e.g.*, a 3' terminator region to increase mRNA stability of the mRNA, such as the PI-II terminator region of potato or the octopine or nopaline synthase 3' terminator regions.

Finally, as noted above, plant expression vectors may also include dominant selectable marker genes to allow for the ready selection of transformants. Such genes include those encoding antibiotic resistance genes (*e.g.*, resistance to hygromycin, kanamycin, bleomycin, G418, streptomycin or spectinomycin) and herbicide resistance genes (*e.g.*, phosphinothricin acetyltransferase).

A reduction of TF expression in a transgenic plant to modify a plant trait may be obtained by introducing into plants antisense constructs based on the TF cDNA. For antisense suppression, the TF cDNA is arranged in reverse orientation relative to the promoter sequence in the expression vector. The introduced sequence need not be the full length TF cDNA or gene, and need not be identical to the TF cDNA or a gene found in the plant type to be transformed. Generally, however, where the introduced sequence is of shorter length, a higher degree of homology to the native TF sequence will be needed for effective antisense suppression. Preferably, the introduced antisense sequence in the vector will be at least 30 nucleotides in length, and improved antisense suppression will typically be observed as the length of the antisense sequence increases. Preferably, the length of the antisense sequence in the vector will be greater than 100 nucleotides. Transcription of an antisense construct as described results in the production of RNA molecules that are the reverse complement of mRNA molecules transcribed from the endogenous TF gene in the plant cell. Suppression of endogenous TF

gene expression can also be achieved using a ribozyme. Ribozymes are synthetic RNA molecules that possess highly specific endoribonuclease activity. The production and use of ribozymes are disclosed in U.S. Patent No. 4,987,071 to Cech and U.S. Patent No. 5,543,508 to Haselhoff. The inclusion of ribozyme sequences within antisense RNAs may be used to confer RNA cleaving activity on the antisense RNA, such that endogenous mRNA molecules that bind to the antisense RNA are cleaved, which in turn leads to an enhanced antisense inhibition of endogenous gene expression.

Vectors in which RNA encoded by the TF cDNA (or variants thereof) is over-expressed may also be used to obtain co-suppression of the endogenous TF gene in the manner described in U.S. Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire TF cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous TF gene. However, as with antisense suppression, the suppressive efficiency will be enhanced as (1) the introduced sequence is lengthened and (2) the sequence similarity between the introduced sequence and the endogenous TF gene is increased.

Vectors expressing an untranslatable form of the TF mRNA may also be used to suppress the expression of endogenous TF activity to modify a trait. Methods for producing such constructs are described in U.S. Patent No. 5,583,021 to Dougherty et al. Preferably, such constructs are made by introducing a premature stop codon into the TF gene. Alternatively, a plant trait may be modified by gene silencing using double-strand RNA (Sharp (1999) *Genes and Development* 13: 139-141).

Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a TF gene. Mutants containing a single mutation event at the desired gene may be crossed to generate homozygous plants for the mutation (Koncz et al. (1992) *Methods in Arabidopsis Research*. World Scientific).

A plant trait may also be modified by using the cre-lox system (for example, as described in US Pat. No. 5,658,772). A plant genome may be modified to include first and second lox sites that are then contacted with a Cre recombinase. If the lox sites are in the same orientation, the intervening DNA sequence between the two sites

is excised. If the lox sites are in the opposite orientation, the intervening sequence is inverted.

The polynucleotides and polypeptides of this invention may also be expressed in a plant in the absence of an expression cassette by manipulating the activity or expression level of the endogenous gene by other means. For example, by ectopically expressing a gene by T-DNA activation tagging (Ichikawa et al., (1997) *Nature* 390 698-701, Kakimoto et al., (1996) *Science* 274: 982-985). This method entails transforming a plant with a gene tag containing multiple transcriptional enhancers and once the tag has inserted into the genome, expression of a flanking gene coding sequence becomes deregulated. In another example, the transcriptional machinery in a plant may be modified so as to increase transcription levels of a polynucleotide of the invention (See PCT Publications WO9606166 and WO 9853057 which describe the modification of the DNA binding specificity of zinc finger proteins by changing particular amino acids in the DNA binding motif).

4. Transgenic Plants with Modified TF Expression

Once an expression cassette comprising a polynucleotide encoding a TF gene of this invention has been constructed, standard techniques may be used to ectopically express the polynucleotide in a plant in order to modify a trait of the plant. The plant may be any higher plant, including gymnosperms, monocotyledonous and dicotyledonous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcubitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al. (1984) *Handbook of Plant Cell Culture –Crop Species*. Macmillan Publ. Co. Shimamoto et al. (1989) *Nature* 338:274-276; Fromm et al. (1990) *Bio/Technology* 8:833-839; and Vasil et al. (1990) *Bio/Technology* 8:429-434.

Transformation and regeneration of both monocotyledonous and dicotyledonous plant cells is now routine, and the selection of the most appropriate transformation technique will be determined by the practitioner. The choice of method will vary with the type of plant to be transformed; those skilled in the art will recognize the suitability of particular methods for given plant types. Suitable

methods may include, but are not limited to: electroporation of plant protoplasts; liposome-mediated transformation; polyethylene glycol (PEG) mediated transformation; transformation using viruses; micro-injection of plant cells; micro-projectile bombardment of plant cells; vacuum infiltration; and *Agrobacterium tumefaciens* mediated transformation. Transformation means introducing a nucleotide sequence in a plant in a manner to cause stable or transient expression of the sequence.

Successful examples of the modification of plant characteristics by transformation with cloned sequences which serve to illustrate the current knowledge in this field of technology, and which are herein incorporated by reference, include: U.S. Patent Nos. 5,571,706; 5,677,175; 5,510,471; 5,750,386; 5,597,945; 5,589,615; 5,750,871; 5,268,526; 5,780,708; 5,538,880; 5,773,269; 5,736,369 and 5,610,042.

Following transformation, plants are preferably selected using a dominant selectable marker incorporated into the transformation vector. Typically, such a marker will confer antibiotic or herbicide resistance on the transformed plants, and selection of transformants can be accomplished by exposing the plants to appropriate concentrations of the antibiotic or herbicide.

After transformed plants are selected and grown to maturity, those plants showing a modified trait are identified. The modified trait may be any of those traits described above. Additionally, to confirm that the modified trait is due to changes in expression levels or activity of the polypeptide or polynucleotide of the invention may be determined by analyzing mRNA expression using Northern blots, RT-PCR or microarrays, or protein expression using immunoblots or Western blots or gel shift assays.

5. Other Utility of the Polypeptide and Polynucleotide Sequences

A transcription factor provided by the present invention may also be used to identify exogenous or endogenous molecules that may affect expression of the transcription factors and may affect any of the traits/phenotypes described herein. These molecules may include organic or inorganic compounds.

For example, the method may entail first placing the molecule in contact with a plant or plant cell. The molecule may be introduced by topical administration, such as spraying or soaking of a plant, and then the molecule's

effect on the expression or activity of the TF polypeptide or the expression of the polynucleotide monitored. Changes in the expression of the TF polypeptide may be monitored by use of polyclonal or monoclonal antibodies, gel electrophoresis or the like. Changes in the expression of the corresponding polynucleotide sequence may be detected by use of microarrays, Northern or any other technique for monitoring changes in mRNA expression. These techniques are exemplified in Ausubel et al. (eds) *Current Protocols in Molecular Biology*, John Wiley & Sons (1998). Such changes in the expression levels may be correlated with modified plant traits and thus identified molecules may be useful for soaking or spraying on fruit, vegetable and grain crops to modify traits in plants.

The transcription factors may also be employed to identify promoter sequences with which they may interact. After identifying a promoter sequence, interactions between the transcription factor and the promoter sequence may be modified by changing specific nucleotides in the promoter sequence or specific amino acids in the transcription factor that interact with the promoter sequence to alter a plant trait. Typically, transcription factor DNA binding sites are identified by gel shift assays. After identifying the promoter regions, the promoter region sequences may be employed in double-stranded DNA arrays to identify molecules that affect the interactions of the TFs with their promoters (Bulyk et al. (1999) *Nature Biotechnology* 17:573-577).

The identified transcription factors are also useful to identify proteins that modify the activity of the transcription factor. Such modification may occur by covalent modification, such as by phosphorylation, or by protein-protein (homo or heteropolymer) interactions. Any method suitable for detecting protein-protein interactions may be employed. Among the methods that may be employed are co-immunoprecipitation, cross-linking and co-purification through gradients or chromatographic columns, and the two-hybrid yeast system.

The two-hybrid system detects protein interactions in vivo and is described in Chien, et al., (1991), *Proc. Natl. Acad. Sci. USA*, 88, 9578-9582 and is commercially available from Clontech (Palo Alto, Calif.). In such a system, plasmids are constructed that encode two hybrid proteins: one consists of the DNA-binding domain of a transcription activator protein fused to the TF polypeptide and the other consists of the transcription activator protein's activation domain fused to an unknown protein that is encoded by a cDNA that has been

recombined into the plasmid as part of a cDNA library. The DNA-binding domain fusion plasmid and the cDNA library are transformed into a strain of the yeast *Saccharomyces cerevisiae* that contains a reporter gene (e.g., lacZ) whose regulatory region contains the transcription activator's binding site. Either hybrid protein alone cannot activate transcription of the reporter gene. Interaction of the two hybrid proteins reconstitutes the functional activator protein and results in expression of the reporter gene, which is detected by an assay for the reporter gene product. Then, the library plasmids responsible for reporter gene expression are isolated and sequenced to identify the proteins encoded by the library plasmids. After identifying proteins that interact with the transcription factors, assays for compounds that interfere with the TF protein-protein interactions may be preformed.

The following examples are intended to illustrate but not limit the present invention.

Example I. Full Length Gene Identification and Cloning

Putative transcription factor sequences (genomic or ESTs) related to known transcription factors were identified in the *Arabidopsis thaliana* GenBank database using the tblastn sequence analysis program using default parameters and a P-value cutoff threshold of -4 or -5 or lower, depending on the length of the query sequence. Putative transcription factor sequence hits were then screened to identify those containing particular sequence strings. If the sequence hits contained such sequence strings, the sequences were confirmed as transcription factors.

As an example, members of the MYB transcription factor family were identified as such if they had one of the following sequence strings:

- a) LRWXNYLRPXXRGXFXEEXIXLHXGNXWSXIXAXLPXGXR,
- b) LRWXNYLRPXXKRGXFXXXEEXIXXXLHXXXGNXWSXIA,
- c) KGXWXXEEDXXL, or
- d) LRWXNYLRPXXXXGXXXXEXXXXXLHXXXGNXWXXIAXXLPGR

Alternatively, *Arabidopsis thaliana* cDNA libraries derived from different tissues or treatments, or genomic libraries were screened to identify novel

members of a transcription family using a low stringency hybridization approach. Probes were synthesized using gene specific primers in a standard PCR reaction (annealing temperature 60° C) and labeled with ³²P dCTP using the High Prime DNA Labeling Kit (Boehringer Mannheim). Purified radiolabelled probes were added to filters immersed in Church hybridization medium (0.5 M NaPO₄ pH 7.0, 7% SDS, 1 % w/v bovine serum albumin) and hybridized overnight at 60 °C with shaking. Filters were washed two times for 45 to 60 minutes with 1xSCC, 1% SDS at 60° C.

As an example, the following GID Nos. may be screened with the primers found in Table 3.

Table 3

GID No.	Forward primer	Reverse Primer
G1035	ACTTTGGGTCCTGCGTCTTAATC ATAGT	ATTACAGTTTTACCCCTGCTGCG ATGA
G663	GAAGCCACAATAACCCCTATTC CTC	TACGAAAGAAAAGCCACCCACA ATCT
G867	TGGAATCGAGTAGCGTTGATGA GAGT	AGAAGAAGAGTTGTTACGAGGC GTGA
G1334	ATGCAAACCTGAGGAGCTTTTGT CGCCA	AGGCAGAGTTTCTTACAACACAC ACT
G921	ATCTCTCTCAACTTTCTTCCTCA GCT	AGCTGCTGCTAAAGCTGCTGTAA AGT

To identify additional sequence 5' or 3' of a partial cDNA sequence in a cDNA library, 5' and 3' rapid amplification of cDNA ends (RACE) was performed using the MarathonTM cDNA amplification kit (Clontech, Palo Alto, CA). Generally, the method entailed first isolating poly(A) mRNA, performing first and second strand cDNA synthesis to generate double stranded cDNA, blunting cDNA ends, followed by ligation of the MarathonTM Adaptor to the cDNA to form a library of adaptor-ligated ds cDNA. Gene-specific primers were designed to be used along with adaptor specific primers for both 5' and 3' RACE reactions. Nested primers, rather than single primers, were used to increase PCR specificity. Using 5' and 3' RACE reactions, 5' and 3' RACE fragments were obtained,

sequenced and cloned. The process may be repeated until 5' and 3' ends of the full-length gene were identified. Then the full-length cDNA was generated by PCR using primers specific to 5' and 3' ends of the gene by end-to-end PCR.

5 **Example IIa Pathogen Resistance Genes**

The sequences shown in Table 4 were identified as being induced during exposure to pathogens.

RT-PCR experiments were performed to identify those genes induced after exposure to biotrophic fungal pathogens, such as *Erysiphe orontii*, necrotrophic fungal pathogens, such as *Fusarium oxysporum*, and salicylic acid which is involved in a nonspecific resistance response in *Arabidopsis thaliana*. The gene expression patterns from ground plant tissue were investigated.

Fusarium oxysporum isolates cause vascular wilts and damping off of various annual vegetables, perennials and weeds (Mauch-Mani and Slusarenko (1994) Molecular Plant-Microbe Interactions 7: 378-383). For *Fusarium oxysporum* experiments, plants grown on petri dishes were sprayed with a fresh spore suspension of *F. oxysporum*. The spore suspension was prepared as follows: A plug of fungal hyphae from a plate culture was placed on a fresh potato dextrose agar plate and allowed to spread for one week. 5 ml sterile water was then added to the plate, swirled, and pipetted into 50 ml Armstrong Fusarium medium. Spores were grown overnight in Fusarium medium and then sprayed onto plants using a Preval paint sprayer. Plant tissue was harvested and frozen in liquid nitrogen 48 hours post infection

Erysiphe orontii is a causal agent of powdery mildew. For *Erysiphe orontii* experiments, plants were grown approximately 4 weeks in a greenhouse under 12 hour light (20 C, ~30% relative humidity (rh)). Individual leaves were infected with *E. orontii* spores from infected plants using a camel's hair brush, and the plants were transferred to a Percival growth chamber (20 C, 80% rh.). Plant tissue was harvested and frozen in liquid nitrogen 7 days post infection.

For salicylic acid experiments, 15 day old seedlings grown on petri dishes were transferred to plates containing 0.5 mM salicylic acid (SA). After 72 hours, leaves were harvested and frozen in liquid nitrogen.

Reverse transcriptase PCR was done using gene specific primers within the coding region for each sequence identified. The primers were designed near the 3' region of each coding sequence initially identified.

5 Total RNA from these tissues were isolated using the CTAB extraction protocol. Once extracted total RNA was normalized in concentration across all the tissue types to ensure that the PCR reaction for each tissue received the same amount of cDNA template using the 28S band as reference. Poly A+ was purified using a modified protocol from the Qiagen Oligotex kit batch protocol. cDNA was synthesized using standard protocols. After the first strand cDNA synthesis, 10 primers for Actin 2 were used to normalize the concentration of cDNA across the tissue types. Actin 2 is found to be constitutively expressed in fairly equal levels across the tissue types we are investigating.

For RT PCR, cDNA template was mixed with corresponding primers and Taq polymerase. Each reaction consisted of 0.2 ul cDNA template, 2ul 10X Tricine buffer, 2 ul 10X Tricine buffer and 16.8 ul water, 0.05ul Primer 1, 0.05 ul, 15 Primer 2, 0.3 ul Taq polymerase and 8.6 ul water.

The 96 well plate was covered with microfilm and set in the Thermocycler to start the following reaction cycle. Step1 93° C for 3 mins, Step 2 93° C for 30 sec, Step 3 65° C for 1 min, Step 4 72° C for 2 mins,. Steps 2, 3 and 4 were 20 repeated for 28 cycles, Step 5 72° C for 5 mins and Step 6 4° C. The PCR plate was placed back in the thermocycler to amplify more products at 8 more cycles to identify genes that have very low expression. The reaction cycle was as follows: Step 2 93° C for 30 sec, Step 3 65° C for 1 min, and Step 4 72° C for 2 ins, repeated for 8 cycles, and Step 4 4° C.

25 8ul of PCR product and 1.5 ul of loading dye were loaded on a 1.2% agarose gel for analysis after 28 cycles and 36 cycles. Expression levels of specific transcripts were considered low if they were only detectable after 36 cycles of PCR. Expression levels were considered medium or high depending on the levels of transcript compared with observed transcript levels for actin2.

30 The transcript levels were upregulated in three repeat experiments whereas in control experiments lower transcript levels were detectable.

Table 4

SEQ ID No.	GID No.	Expression Induced by:
SEQ ID No. 43	G663 (MYB)	<i>Fusarium</i> , SA
SEQ ID No. 17	G867 (AP2)	<i>Erysyphe</i>
SEQ ID No. 83	G920 (WRKY)	<i>Erysyphe</i> , SA
SEQ ID No. 85	G921 (WRKY)	<i>Fusarium</i> , <i>Erysyphe</i> , SA
SEQ ID No. 129	G1334 (CAAT)	SA
SEQ ID No. 87	G986 (WRKY)	<i>Erysyphe</i>
SEQ ID No. 91	G1043 (WRKY)	<i>Erysyphe</i>
SEQ ID No. 1061	G1048 (bZIP)	<i>Erysyphe</i>

Example IIb. Environmental Stress Genes

The sequences shown in Table 5 were identified as being induced during exposure to an environmental stress.

RT-PCR experiments using treated rosette leaf tissue were performed as described above to identify those genes induced after exposure of the plants or seedlings to chilling stress (6 hour exposure to 4° C), heat stress (6 hour exposure to 37° C), high salt stress (6 hour exposure to 200 mM NaCl), drought stress (168 hours after removing water from trays), osmotic stress (6 hour exposure to 3 M mannitol), hormones (6 hours after spraying plants with 1 uM indole acetic acid (2,4-D) or 50 uM abscissic acid (ABA)). The gene expression patterns from ground plant leaf tissue was investigated as described above.

The transcript levels were upregulated in seven experiments whereas in control experiments lower levels were observed.

Table 5

SEQ ID No.	GID No.	Expression Induced by:
SEQ ID No. 9	G10 (AP2)	2,4-D; Cold
SEQ ID No. 43	G663 (MYB)	2,4-D; ABA; Cold; Drought; Osmotic
SEQ ID No. 17	G867 (AP2)	2,4-D; Cold
SEQ ID No. 85	G921 (WRKY)	All, but salt
SEQ ID No. 27	G975 (AP2)	Cold; Drought
SEQ ID No. 65	G1328 (MYB)	ABA; Osmotic

SEQ ID No. 129	G1334 (CAAT)	Heat; Drought
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Example IIc. Seed or Root Active Genes

5 The sequences in Table 6 were expressed at higher levels in seeds or roots compared with other plant tissue.

For preparation of seed tissue the following protocol was used. About 10-20g of frozen siliques were poured into a chilled pestle. The frozen siliques were repeatedly tapped and occasionally very lightly ground with a pestle. After several
10 minutes of the tapping procedure, the broken, frozen siliques were poured through a pre-chilled fine mesh sieve made of metal, into another chilled mortar containing a small amount of liquid nitrogen assuring that the broken material was completely frozen but free of liquid nitrogen before beginning the pouring and sifting process. After the sieve has been filled with the broken material, lightly tap the edge of the
15 sieve to cause the immature seeds to fall through the mesh into the liquid nitrogen (at this point, small pieces of contaminating tissue will also pass through the sieve). This process was repeated until almost all of the siliques were broken open, and very few attached immature seeds were visible. The harvested immature seeds can then be filtered several times through the sieve to further remove contaminating
20 tissue. The immature seeds were stored at -80° C until further use once the seeds contained less than 1-2% contaminating tissue.

RT-PCR experiments were performed as described above.

Table 6

SEQ ID No.	GID No.	Activity
SEQ ID No. 9	G10 (AP2)	Root
SEQ ID No. 17	G867 (AP2)	Root
SEQ ID No. 3	G5 (AP2)	Root
SEQ ID No. 35	G993 (AP2)	Root
SEQ ID No. 125	G699 (HB)	Root
SEQ ID No. 93	G1091 (WRKY)	Root
SEQ ID No. 57	G932 (MYB)	Seed
SEQ ID No. 67	G858 (MADS)	Seed

SEQ ID No. 21	G872 (AP2)	Seed
SEQ ID No. 97	G838 (AKR)	Seed
SEQ ID No. 43	G663 (MYB)	Seed
SEQ ID No. 159	G1035 (bZIP)	Seed
SEQ ID No. 135	G462 (IAA/AUX)	Shoots

Example IV. Construction of Expression Vectors

The sequence was amplified from a genomic or cDNA library using primers specific to sequences upstream and downstream of the coding region. The expression vector was pMEN001, which is derived from pBin19 (Bevan M (1984) *Nucleic Acids Research* 12:8711-8720). To clone the sequence into the vector, both pMEN001 and the genomic sequence clone were digested separately with Sall and XbaI restriction enzymes at 37° C for 2 hours. The digestion products were subject to electrophoresis in a 0.8% agarose gel and visualized by ethidium bromide staining. The DNA fragments containing the sequence and the linearized plasmid were excised and purified by using a Qiaquick gel extraction kit (Qiagen, CA). The fragments of interest were ligated at a ratio of 3:1 (vector to insert). Ligation reactions using T4 DNA ligase (New England Biolabs, MA) were carried out at 16° C for 16 hours. The ligated DNAs were transformed into competent cells of the *E. coli* strain DH5alpha by using the heat shock method. The transformations were plated on LB plates containing 50 mg/l kanamycin (Sigma).

Individual colonies were grown overnight in five milliliters of LB broth containing 50 mg/l kanamycin at 37° C. Plasmid DNA was purified by using Qiaquick Mini Prep kits (Qiagen, CA).

Example V. Transformation of *Agrobacterium* with the Expression Vector

After the plasmid vector containing the gene was constructed, the vector was used to transform *Agrobacterium tumefaciens* cells expressing the gene products. The stock of *Agrobacterium tumefaciens* cells for transformation were made as described by Nagel et al. *FEMS Microbiol Letts* 67: 325-328 (1990). *Agrobacterium* strain GV3101 was grown in 250 ml LB medium (Sigma) overnight at 28°C with shaking until an absorbance (A_{600}) of 0.5 – 1.0 was reached. Cells were harvested by centrifugation at 4,000 x g for 15 min at 4° C. Cells were

then resuspended in 250 µl chilled buffer (1 mM HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 µl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended cells were then distributed into 40 µl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Agrobacterium cells were transformed with plasmids prepared as described above following the protocol described by Nagel et al. *FEMS Microbiol Letts* 67: 325-328 (1990). For each DNA construct to be transformed, 50 – 100 ng DNA (generally resuspended in 10 mM Tris-HCl, 1 mM EDTA, pH 8.0) was mixed with 40 µl of *Agrobacterium* cells. The DNA/cell mixture was then transferred to a chilled cuvette with a 2mm electrode gap and subject to a 2.5 kV charge dissipated at 25 µF and 200 µF using a Gene Pulser II apparatus (Bio-Rad). After electroporation, cells were immediately resuspended in 1.0 ml LB and allowed to recover without antibiotic selection for 2 – 4 hours at 28° C in a shaking incubator. After recovery, cells were plated onto selective medium of LB broth containing 100 µg/ml spectinomycin (Sigma) and incubated for 24-48 hours at 28° C. Single colonies were then picked and inoculated in fresh medium. The presence of the plasmid construct was verified by PCR amplification and sequence analysis.

Example VI. Transformation of *Arabidopsis* Plants with *Agrobacterium tumefaciens* with Expression Vector

After transformation of *Agrobacterium tumefaciens* with plasmid vectors containing the gene, single *Agrobacterium* colonies were identified, propagated, and used to transform *Arabidopsis* plants. Briefly, 500 ml cultures of LB medium containing 50 mg/l kanamycin were inoculated with the colonies and grown at 28° C with shaking for 2 days until an absorbance (A_{600}) of > 2.0 is reached. Cells were then harvested by centrifugation at 4,000 x g for 10 min, and resuspended in infiltration medium (1/2 X Murashige and Skoog salts (Sigma), 1 X Gamborg's B-5 vitamins (Sigma), 5.0% (w/v) sucrose (Sigma), 0.044 µM benzylamino purine (Sigma), 200 µl/L Silwet L-77 (Lehle Seeds) until an absorbance (A_{600}) of 0.8 was reached.

Prior to transformation, *Arabidopsis thaliana* seeds (ecotype Columbia) were sown at a density of ~10 plants per 4" pot onto Pro-Mix BX potting medium

(Hummert International) covered with fiberglass mesh (18 mm X 16 mm). Plants were grown under continuous illumination (50-75 $\mu\text{E}/\text{m}^2/\text{sec}$) at 22-23° C with 65-70% relative humidity. After about 4 weeks, primary inflorescence stems (bolts) are cut off to encourage growth of multiple secondary bolts. After flowering of the mature secondary bolts, plants were prepared for transformation by removal of all siliques and opened flowers.

The pots were then immersed upside down in the mixture of *Agrobacterium* infiltration medium as described above for 30 sec, and placed on their sides to allow draining into a 1' x 2' flat surface covered with plastic wrap. After 24 h, the plastic wrap was removed and pots are turned upright. The immersion procedure was repeated one week later, for a total of two immersions per pot. Seeds were then collected from each transformation pot and analyzed following the protocol described below.

15 **Example VII. Identification of Arabidopsis Primary Transformants**

Seeds collected from the transformation pots were sterilized essentially as follows. Seeds were dispersed into in a solution containing 0.1% (v/v) Triton X-100 (Sigma) and sterile H₂O and washed by shaking the suspension for 20 min. The wash solution was then drained and replaced with fresh wash solution to wash the seeds for 20 min with shaking. After removal of the second wash solution, a solution containing 0.1% (v/v) Triton X-100 and 70% ethanol (Equistar) was added to the seeds and the suspension was shaken for 5 min. After removal of the ethanol/detergent solution, a solution containing 0.1% (v/v) Triton X-100 and 30% (v/v) bleach (Clorox) was added to the seeds, and the suspension was shaken for 10 min. After removal of the bleach/detergent solution, seeds were then washed five times in sterile distilled H₂O. The seeds were stored in the last wash water at 4° C for 2 days in the dark before being plated onto antibiotic selection medium (1 X Murashige and Skoog salts (pH adjusted to 5.7 with 1M KOH), 1 X Gamborg's B-5 vitamins, 0.9% phytagar (Life Technologies), and 50 mg/l kanamycin). Seeds were germinated under continuous illumination (50-75 $\mu\text{E}/\text{m}^2/\text{sec}$) at 22-23° C. After 7-10 days of growth under these conditions, kanamycin resistant primary transformants (T₁ generation) were visible and obtained. These seedlings were transferred first to fresh selection plates where the seedlings continued to grow for 3-5 more days, and then to soil (Pro-Mix BX potting medium).

Primary transformants are crossed and progeny seeds (T₂) collected; kanamycin resistant seedlings are selected and analyzed as described above.

Example VIIIa. Pathogen Resistance or Tolerance in Transgenic Plants

5 Pathogen resistance or pathogen tolerance in a transgenic *Arabidopsis* plant is compared with that of a wild type plant.

Two week old *Arabidopsis* seedlings are inoculated with *Fusarium* by spraying with a spore suspension (2×10^6 conidia per millimeter) and incubated under high humidity. Plants are then scored macroscopically for disease symptoms or microscopically for fungal growth or using microarrays for the induction of resistance associated genes (such as the defensin genes) to detect resistance or tolerance of the plant tissue. A wild type plant should show the first signs of damage (gradual yellowing of leaves, damping off of seedlings or growth of fungal mycelium) after four days from inoculation. Wild type resistant ecotypes should show some damage after 2 weeks. Transgenic plants which are pathogen tolerant should show the initial symptoms between 4 days and 2 weeks. Transgenic plants (from a nonresistant phenotype) which are pathogen resistant should show initial signs of damage, if any, after 2 weeks.

Erysiphe inoculations are done by tapping conidia from 1 to 2 heavily infected leaves onto the mesh cover of a settling tower, brushing the mesh with a camel's hair paint brush to break up the conidial chains, and letting the conidia settle for 10 minutes. Plants are 4 to 4.5 weeks old at the time of inoculation. Spores are obtained from 10 to 14 day old *Erysiphe* cultures. The mesh has a pore size of 95 microns; the settling towers are 28" high, and wide enough to fit over a box of plants (6"x6" or 6"x8"). Symptoms are evaluated 7 –21 days post-inoculation. Typically, within the first twenty-four hours, the spores differentiate into several fungal structures including the haustorium that invaginates a host's epidermal plasma membrane. Formation of aerial mycelium and sporulation represent late differentiation events between 4 and 7 days post inoculation (Freilaldenhoven et al. (1994) *Plant Cell* 6: 983-994). Events associated with resistance or tolerance to the pathogen includes: the induction of pathogen resistance related genes (R genes), the activation of cell death in the attacked epidermal cells (hypersensitive response), the induction of certain chemicals, such as phytoalexins, and the lignification that occurs at attempted penetration sites.

Assays are performed to observe these events. Transgenic plants are identified that induce R genes, activate cell death, induce chemicals or increase lignification sooner or to a greater extent than wild type plants when exposed to A pathogen.

5 These transgenic plants may be more resistant to biotrophic or necrotrophic pathogens such as a fungus, bacterium, mollicute, virus, nematode, a parasitic higher plant or the like and associated diseases. In particular, pathogens such as *Fusarium oxysporum*, *Erysiphe orontii* and other powdery mildews, *Sclerotinia spp.*, soil-borne oomycetes, foliar oomycetes, *Botrytis spp.*, *Rhizoctonia spp.*, *Verticillium dahliae/albo-atrum*, *Alternaria spp.*, rusts, *Mycosphaerella spp.*, *Fusarium solani*, or the like. The diseases include fungal diseases such as rusts, smuts, wilts, yellows, root rot, leaf drop, ergot, leaf blight of potato, brown spot of rice, leaf blight, late blight, powdery mildew, downy mildew, and the like; viral diseases such as sugarcane mosaic, cassava mosaic, sugar beet yellows, plum pox, barley yellow dwarf, tomato yellow leaf curl, tomato spotted wilt virus, and the like; bacterial diseases such as citrus canker, bacterial leaf blight, bacterial wilt, soft rot of vegetables, and the like; nematode diseases such as root knot, sugar beet cyst nematode or the like.

Example VIIIb. Seed or Root Trait Modification

20 Transgenic plants are identified that ectopically express those transcription factors that are active in seed or roots. These plants may have improved seed germination characteristics; shelf-life; seed drydown characteristics; size; stress responses, such as to heat, chilling, freezing, high salt or osmotic shock; protein, oil or starch content; other nutritional content, such as vitamins, minerals, flavonoids, phytosterols or phytic acid; seedling vigor; insect resistance, or seed coat quality. The same or other plants may have improved root characteristics such as root hair number, stress responses, in particular to drought, root length, pest resistance, absorption of nutrients, such as nitrogen and phosphorus containing compounds, or the like.

Example VIIIc. Other Trait Modifications

Transgenic plants overexpressing the identified TF genes are shown with observed trait modifications in Table 7.

Table 7

SEQ ID No.	GID No. (Family)	Phenotype
SEQ ID No. 151	G629 (bZIP)	Tolerant to potassium deficiency
SEQ ID No. 153	G630 (bZIP)	Increased insoluble sugar
SEQ ID No. 123	G399 (HB)	More sensitive to high osmotic conditions, more beta-carotene and lutein, oil content modified
SEQ ID No. 125	G699 (HB)	More tolerant to high osmotic conditions
SEQ ID No. 127	G964 (HB)	Modifies normal responses to temperature, better germination in heat, early flowering
SEQ ID No. 43	G663 (MYB)	High pigment, increased fatty acid content, growth regulator, modified sensitivity to ethylene, pathogen resistance
SEQ ID No. 45	G664 (MYB)	More rapid growth and germination, modified responses to temperature, tolerant to potassium deficiency
SEQ ID No. 47	G672 (MYB)	Tolerant to high salt
SEQ ID No. 117	G911 (Z)	Tolerant to potassium deficiency
SEQ ID No. 19	G869 (AP2)	Modified flowering response
SEQ ID No. 37	G1020 (AP2)	Modified flowering response
SEQ ID No. 157	G1034 (bZIP)	Modified ethylene sensitivity
SEQ ID No. 137	G782 (HLH/MYC)	Tolerance to increased osmotic pressure
SEQ ID No. 139	G783 (HLH/MYC)	Tolerance to increased osmotic pressure
SEQ ID No. 105	G751 (Z)	Modified sensitivity to ethylene

Those transgenic plants with trait modifications associated with germination, flowering time are useful for reducing breeding time for crops, allowing long generation time plants such as trees to propagate faster, and reducing generation time for crops to allow more harvests per growing season. Those

transgenic plants with altered flowering times may also be employed for delaying flowering to allow more vegetative grow to increase yield. e.g. sugarbeet, regulating the vernalization process to allow growth of high yield winter crops in warmer regions, preventing vegetative crops from flowering hence reducing the possibility of pollen escape for genetically modified organisms, altering the architecture of plants for better vegetative growth or for ornamental plants, synchronizing blooming time using a inducible system, or reducing frost damage to blossom by delaying the flower time and induce later.

Those transgenic plants exhibiting a modified uptake of micronutrients are useful for growing plants in areas where such micronutrients are deficient or to minimize the use of fertilizers. Those transgenic plants able to withstand higher osmotic pressure or high salt are useful for growth in more arid conditions than normal for the wild type plant and may be more able to survive drought conditions. Those transgenic plants exhibiting a modified carotene or oil content are useful for increasing the nutritional value of the plant.

Example IX. Transformation of Cereal Plants with the Expression Vector

A cereal plant, such as corn, wheat, rice, sorghum or barley, can also be transformed with the plasmid vectors containing the sequence and constitutive or inducible promoters to modify a trait. In these cases, a cloning vector, pMEN020, is modified to replace the NptII coding region with the BAR gene of *Streptomyces hygroscopicus* that confers resistance to phosphinothricin. The KpnI and BglII sites of the Bar gene are removed by site-directed mutagenesis with silent codon changes.

Plasmids according to the present invention may be transformed into corn embryogenic cells derived from immature scutellar tissue by using microprojectile bombardment, with the A188XB73 genotype as the preferred genotype (Fromm et al., *Bio/Technology* 8: 833-839 (1990); Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)). After microprojectile bombardment the tissues are selected on phosphinothricin to identify the transgenic embryogenic cells (Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)). Transgenic plants are regenerated by standard corn regeneration techniques (Fromm, et al., *Bio/Technology* 8: 833-839 (1990); Gordon-Kamm et al., *Plant Cell* 2: 603-618 (1990)).

Example X. Identification of Homologous Sequences

Homologs from the same plant, different plant species or other organisms were identified using database sequence search tools, such as the Basic Local Alignment Search Tool (BLAST) (Altschul et al. (1990) *J. Mol. Biol.* 215:403-410; and Altschul et al. (1997) *Nucl. Acid Res.* 25: 3389-3402). The tblastn or blastn sequence analysis programs were employed using the BLOSUM-62 scoring matrix (Henikoff, S. and Henikoff, J. G. (1992) *Proc. Natl. Acad. Sci. USA* 89: 10915-10919). The output of a BLAST report provides a score that takes into account the alignment of similar or identical residues and any gaps needed in order to align the sequences. The scoring matrix assigns a score for aligning any possible pair of sequences. The P values reflect how many times one expects to see a score occur by chance. Higher scores are preferred and a low threshold P value threshold is preferred. These are the sequence identity criteria. The tblastn sequence analysis program was used to query a polypeptide sequence against six-way translations of sequences in a nucleotide database. Hits with a P value less than -25, preferably less than -70, and more preferably less than -100, were identified as homologous sequences. The blastn sequence analysis program was used to query a nucleotide sequence against a nucleotide sequence database. In this case too, higher scores were preferred and a preferred threshold P value was less than -13, preferably less than -50, and more preferably less than -100.

Alternatively, a fragment of a sequence from Table 1 is ³²P-radiolabeled by random priming (Sambrook et al., (1989) *Molecular Cloning. A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, New York) and used to screen a plant genomic library. As an example, total plant DNA from *Arabidopsis thaliana*, *Nicotiana tabacum*, *Lycopersicon pimpinellifolium*, *Prunus avium*, *Prunus cerasus*, *Cucumis sativus*, or *Oryza sativa* are isolated according to Stockinger al (Stockinger, E. J., et al., (1996), *J. Heredity*, 87:214-218). Approximately 2 to 10 µg of each DNA sample are restriction digested, transferred to nylon membrane (Micron Separations, Westboro, MA) and hybridized. Hybridization conditions are: 42° C in 50% formamide, 5X SSC, 20 mM phosphate buffer 1X Denhardt's, 10% dextran sulfate, and 100µg/ml herring sperm DNA. Four low stringency washes at RT in 2X SSC, 0.05% sodium sarcosyl and 0.02% sodium pyrophosphate are performed prior to high stringency washes at 55° C in 0.2X

SSC, 0.05% sodium sarcosyl and 0.01% sodium pyrophosphate. High stringency washes are performed until no counts are detected in the washout according to Walling et al. (Walling, L. L., et al., (1988) Nucl. Acids Res. 16:10477-10492).

5 All references (publications and patents) are incorporated herein by reference in their entirety for all purposes.

Although the invention has been described with reference to the embodiments and examples above, it should be understood that various modifications can be made without departing from the spirit of the invention.
10 Accordingly, the invention is limited only by the following claims.

We Claim:

5 1. An isolated polynucleotide comprising a nucleotide sequence
selected from the group consisting of: (a) a nucleotide sequence encoding a
polypeptide comprising a sequence selected from the group consisting of SEQ ID
Nos. 2N-1, where N= 1-85; (b) a nucleotide sequence encoding a polypeptide
10 comprising a sequence selected from the group consisting of SEQ ID Nos. 2N-1,
where N= 1-85; including substitutions, deletions or insertions; (c) a nucleotide
sequence encoding a fragment from a polypeptide of (a) or (b); (d) a nucleotide
sequence comprising a sequence selected from the group consisting of SEQ ID
Nos. 2N-1, where N= 1-85; (e) a nucleotide sequence having at least 40% identity
with a nucleotide sequence of (a) or (b); (f) a nucleotide sequence having at least
15 60% identity with a nucleotide sequence of (c); (g) a nucleotide sequence
comprising at least 15 consecutive nucleotides of SEQ ID Nos. 2N-1, where N=1-
85; and (h) a nucleotide sequence that hybridizes to a sequence encoding a
polypeptide of (a), (b) or (c) under stringent conditions.

20 2. The isolated polynucleotide of claim 1, further comprising a
constitutive promoter operably linked to said nucleotide sequence

25 3. The isolated polynucleotide of claim 1, further comprising an
inducible promoter operably linked to said nucleotide sequence.

 4. The isolated polynucleotide of claim 1, further comprising a tissue-
active promoter operably linked to said nucleotide sequence.

30 5. An expression vector comprising an isolated polynucleotide of
claim 1.

 6. A host cell comprising an expression vector of claim 5.

7. A transgenic plant comprising an isolated polynucleotide of claim 1.

8. A transgenic plant ectopically expressing an isolated polynucleotide of claim 1.

5

9. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: (a) a sequence selected from SEQ ID Nos. 2(N), where N= 1-85; (b) a sequence selected from SEQ ID Nos. SEQ ID Nos. 2(N), where N= 1-85; including substitutions, deletions or insertions; (c) a sequence from a fragment from a polypeptide of (a) or (b); (d) a sequence having at least 40% identity with a sequence of (a) or (b); and (e) a sequence having at least 60% identity with a sequence of (a) or (b).

10

10. A transgenic plant ectopically expressing an isolated polypeptide of claim 9.

15

11. A method for screening a molecule to identify a molecule that modifies a plant trait, said method comprising (a) placing the molecule in contact with the plant; and (b) monitoring the effect of the molecule on the expression or activity of a polypeptide of claim 9 or the expression of a polynucleotide of claim 1.

20

12. A method for producing a transgenic plant having a modified trait, said method comprising ectopically expressing the isolated polynucleotide of claim 1 and selecting a plant with the modified trait.

25

13. A method for identifying a sequence homologous to the polynucleotide of claim 1, said method comprising (a) providing a database sequence; (b) aligning and comparing the sequence of the polynucleotide of claim 1 with the database sequence to determine whether the database sequence meets sequence identity criteria relative to the polynucleotide of claim 1; and (c) selecting a database sequence that meets the sequence identity criteria.

30

14. A polynucleotide sequence identified by the method of claim 13.

15. A method for identifying a sequence homologous to the polypeptide of claim 8, said method comprising (a) providing a database sequence; (b) aligning and comparing the sequence of the polypeptide of claim 8 with the database sequence to determine whether the database sequence meets sequence identity criteria relative to the polypeptide of claim 8; and (c) selecting a database sequence that meets the sequence identity criteria.

16. A polypeptide sequence identified by the method of claim 15.

17. A method for screening for a transcription factor that modifies a plant trait, said method comprising (a) generating one or more transgenic plants ectopically expressing an isolated polynucleotide of claim 1 and (b) identifying whether said generated transgenic plant is a plant with a modified plant trait.

ABSTRACT OF THE INVENTION

Compositions and methods are provided for modifying a trait of a plant. Isolated polynucleotide and polypeptide sequences are provided, along with an expression vector comprising the isolated polynucleotide, a host cell comprising the isolated polynucleotide, and a transgenic plant comprising the isolated polynucleotide. Also provided is a method for producing a transgenic plant, a method for screening for a compound that may modify the trait and a method for identifying other homologous polynucleotide and polypeptide sequences.

10

DECLARATION FOR UTILITY PATENT APPLICATION

As a below-named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name;

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

PLANT GENE SEQUENCES I

the specification of which is attached hereto.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information which is material to patentability as defined in Title 37, Code of Federal Regulations, § 1.56(a) which states in relevant part: "Each individual associated with the filing and prosecution of a patent application has a duty of candor and good faith in dealing with the Office, which includes a duty to disclose to the Office all information known to that individual to be material to patentability as defined in this section. The duty to disclose all information known to be material to patentability is deemed to be satisfied if all information known to be material to patentability of any claim issued in a patent was cited by the Office or submitted to the Office in the manner prescribed by §§ 1.97(b)-(d) and 1.98.

I hereby claim foreign priority benefits under Title 35 United States Code, § 119(a)-(d) or 365(a)-(b) of any foreign applications for patent or inventor's certificate as indicated below and have also identified below any foreign application for patent or inventor's certificate having a filing date before that of the application on which priority is claimed:

I hereby claim the benefit of priority under Title 35 United States Code, § 119(e) of any United States provisional application(s) listed below:

Provisional Serial Nos. 60/101,349
60/103,312
60/108,734
60/113,409

Filing Dates:9/22/98
10/6/98
11/17/98
12/22/98

60101349 60103312 60108734 60113409

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Title 18, United States Code, § 1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Title 18, United States Code, §1001 and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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Post Office Address: Same as above.

Inventor's signature:

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Post Office Address: Same as above.

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Full name of fourth joint coinventor: Jose Luis Riechmann

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Date:

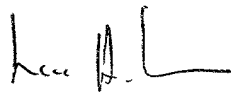
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Full name of fifth joint coinventor: Luc Adam

Inventor's signature:



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Full name of sixth joint coinventor: Pierre Broun

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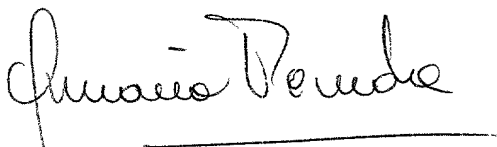
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656160 "6T6T6E6D

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Inventor's signature:

Citizenship: China

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Same as above.

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN RE PATENT APPLICATION OF
Jacqueline Heard et al.

Examiner: Unknown

Group Art Unit: Unknown

Application No. Unassigned

Filing Date: Herewith

Title: Plant Gene Sequences I

POWER OF ATTORNEY BY ASSIGNEE
TO EXCLUSION OF INVENTOR UNDER 37 C.F.R. § 3.71

Commissioner of Patents
and Trademarks
Washington, D.C. 20231

Sir:

The undersigned ASSIGNEE having an interest in the above-identified application for letters patent hereby appoints Karen J. Guerrero, Reg. No. 37,071 to prosecute this application and transact all business in the United States Patent and Trademark Office in connection therewith and hereby revokes all prior powers of attorney; said appointment to be to the exclusion of the inventors and the inventors' attorneys in accordance with the provisions of 37 C.F.R. § 3.71.

The following evidentiary documents establish a chain of title from the original owner to the Assignee:

X a copy of an Assignment attached hereto, which Assignment has been (or is herewith) forwarded to the Patent and Trademark Office for recording; or

- the Assignment recorded on _____ at reel __, frames __ - __.

Pursuant to 37 C.F.R. § 3.73(b) the undersigned Assignee hereby states that evidentiary documents have been reviewed and hereby certifies that, to the best of ASSIGNEE's knowledge and belief, title is in the identified ASSIGNEE.

Direct all telephone calls to Karen J. Guerrero (510) 264-0280 ext. 125.

Address all correspondence to:

Karen J. Guerrero
MENDEL BIOTECHNOLOGY, INC.
21375 Cabot Boulevard
Hayward, California 94545

ASSIGNEE: Mendel Biotechnology, Inc.

Name: *Michael Fromm*

Name:
Michael Fromm

Title:
President and CEO

Date: *9/8/99*

656 T 60 646 640

[illegible]

In re patent application of

Serial No. Unassigned

For: PLANT GENE SEQUENCES I

Assistant Commissioner for Patents
Washington, D.C. 20231
Box SEQUENCE

In connection with a Sequence Listing submitted concurrently herewith, the undersigned hereby states that:

2. the content of the attached paper copy and the attached computer readable copy of the Sequence Listing, submitted in accordance with 37 C.F.R. § 1.821(c) and (e), respectively, are the same; and

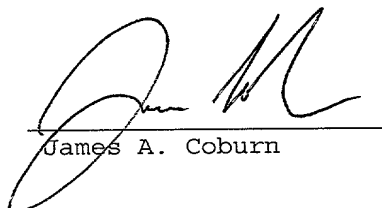
3. all statements made herein of their own knowledge are true and that all statements made on information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United

Serial No. Unassigned

States Code and that such willful false statements may jeopardize the validity of the application or any patent resulting therefrom.

Respectfully submitted,

Aug. 30, 1999
Date


James A. Coburn

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Arg	Ala	Tyr	Asp	Ala	Ala	Ala	Arg	Arg	Ile	Arg	Gly	Thr	Lys	Ala	Lys
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Ala	Ala	Ala	Met	Asn	Leu	Tyr	Thr	Cys	Ser	Arg	Ser	Phe	Gln	Asp	Ser	
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Gly	Gly	Glu	Leu	Met	Asp	Ala	Leu	Val	Pro	Phe	Ile	Lys	Ser	Val	Ser	
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gat	tct	cct	tct	tct	tct	tct	gca	gcg	tct	gcg	tct	gcg	ttt	ctt	cac	563
Asp	Ser	Pro	Ser	Ser	Ser	Ser	Ala	Ala	Ser	Ala	Ser	Ala	Phe	Leu	His	
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Pro	Ser	Ala	Phe	Ser	Leu	Pro	Pro	Leu	Pro	Gly	Tyr	Tyr	Pro	Asp	Ser	
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Gly Ser Leu Ile Gly Leu Asn Asn Leu Ser Ser Ser Gln Ile His Gln	
85 90 95	
atc cag tct cag atc cat cat cct ctt cct ccg acg cat cac aac aac	755
Ile Gln Ser Gln Ile His His Pro Leu Pro Pro Thr His His Asn Asn	
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Asn Asn Ser Phe Ser Asn Leu Leu Ser Pro Lys Pro Leu Leu Met Lys	
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Gln Ser Gly Val Ala Gly Ser Cys Phe Ala Tyr Gly Ser Gly Val Pro	
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Lys Trp Val Ala Glu Ile Arg Leu Pro Arg Asn Arg Thr Arg Leu Trp	
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Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Lys	
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Leu Arg His Asn Gly Phe His Ile Gly Gly Asp Phe Gly Glu Tyr Lys	
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Pro Leu His Ser Ser Val Asp Ala Lys Leu Glu Ala Ile Cys Lys Ser	
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Met Ala Glu Thr Gln Lys Gln Asp Lys Ser Thr Lys Ser Ser Lys Lys	
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cgt gag aag aag gtt tcg tcg cca gat cta tcg gag aaa gtg aag gcg	1235
Arg Glu Lys Lys Val Ser Ser Pro Asp Leu Ser Glu Lys Val Lys Ala	
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Glu Glu Asn Ser Val Ser Ile Gly Gly Ser Pro Pro Val Thr Glu Phe	
275 280 285	

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 Glu Glu Ser Thr Ala Gly Ser Ser Pro Leu Ser Asp Leu Thr Phe Ala
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gac ccg gag gag ccg ccg cag tgg aac gag acg ttc tcg ttg gag aag 1379
 Asp Pro Glu Glu Pro Pro Gln Trp Asn Glu Thr Phe Ser Leu Glu Lys
 310 315 320

tat ccg tcg tac gag atc gat tgg gat tcg att cta gct taggggcaaa 1428
 Tyr Pro Ser Tyr Glu Ile Asp Trp Asp Ser Ile Leu Ala
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His Pro Ser Ala Phe Ser Leu Pro Pro Leu Pro Gly Tyr Tyr Pro Asp
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Ser Thr Phe Leu Thr Gln Pro Phe Ser Tyr Gly Ser Asp Leu Gln Gln
 65 70 75 80

Thr Gly Ser Leu Ile Gly Leu Asn Asn Leu Ser Ser Ser Gln Ile His
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Gln Ile Gln Ser Gln Ile His His Pro Leu Pro Pro Thr His His Asn
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Asn Asn Asn Ser Phe Ser Asn Leu Leu Ser Pro Lys Pro Leu Leu Met
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Gly Lys Trp Val Ala Glu Ile Arg Leu Pro Arg Asn Arg Thr Arg Leu
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Trp Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp
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Lys Ala Ala Tyr Lys Leu Arg Gly Asp Phe Ala Arg Leu Asn Phe Pro
 195 200 205

Asn Leu Arg His Asn Gly Phe His Ile Gly Gly Asp Phe Gly Glu Tyr
 210 215 220

Lys Pro Leu His Ser Ser Val Asp Ala Lys Leu Glu Ala Ile Cys Lys
 225 230 235 240

Ser Met Ala Glu Thr Gln Lys Gln Asp Lys Ser Thr Lys Ser Ser Lys
 245 250 255

Lys Arg Glu Lys Lys Val Ser Ser Pro Asp Leu Ser Glu Lys Val Lys
 260 265 270

Ala Glu Glu Asn Ser Val Ser Ile Gly Gly Ser Pro Pro Val Thr Glu
 275 280 285

Phe Glu Glu Ser Thr Ala Gly Ser Ser Pro Leu Ser Asp Leu Thr Phe
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 cgatcatctc gagctcttcg tgagagatta tgtgattatg taatcgttgt tgctgtagaa 180
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cttgag atg ttg gat ctt aac ctc aac gct gat tct ccc gag tcg act	288
Met Leu Asp Leu Asn Leu Asn Ala Asp Ser Pro Glu Ser Thr	
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Gln Tyr Gly Gly Asp Ser Tyr Leu Asp Arg Gln Thr Ser Asp Asn Ser	
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Ala Gly Asn Arg Val Glu Glu Ser Gly Thr Ser Thr Ser Ser Val Ile	
35 40 45	
aat gcc gat gga gac gaa gac tct tgc tct act cga gct ttc act ctc	432
Asn Ala Asp Gly Asp Glu Asp Ser Cys Ser Thr Arg Ala Phe Thr Leu	
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Ser Phe Asp Ile Leu Lys Val Gly Ser Ser Ser Gly Gly Asp Glu Ser	
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ccc gcc gct tca gct tcc gtt act aaa gag ttt ttt ccg gtg agt gga	528
Pro Ala Ala Ser Ala Ser Val Thr Lys Glu Phe Phe Pro Val Ser Gly	
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gac tgt gga cat cta cga gat gtt gaa gga tca tca agc tct aga aac	576
Asp Cys Gly His Leu Arg Asp Val Glu Gly Ser Ser Ser Ser Arg Asn	
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Trp Ile Asp Leu Ser Phe Asp Arg Ile Gly Asp Gly Glu Thr Lys Leu	
115 120 125	
gta act ccg gtt ccg act ccg gct ccg gtt ccg gct cag gtt aaa aag	672
Val Thr Pro Val Pro Thr Pro Ala Pro Val Pro Ala Gln Val Lys Lys	
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Ser Arg Arg Gly Pro Arg Ser Arg Ser Ser Gln Tyr Arg Gly Val Thr	
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Phe Tyr Arg Arg Thr Gly Arg Trp Glu Ser His Ile Trp Asp Cys Gly	
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Lys Gln Val Tyr Leu Gly Gly Phe Asp Thr Ala His Ala Ala Ala Arg	
175 180 185 190	
gct tat gat cga gct gct att aaa ttt aga ggt gtt gat gct gat atc	864
Ala Tyr Asp Arg Ala Ala Ile Lys Phe Arg Gly Val Asp Ala Asp Ile	
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Asn Phe Thr Leu Gly Asp Tyr Glu Glu Asp Met Lys Gln Val Gln Asn	
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Phe Ser Arg Gly Ser Ser Lys Tyr Arg Gly Val Thr Leu His Lys Cys	
240 245 250	
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Gly Arg Trp Glu Ala Arg Met Gly Gln Phe Leu Gly Lys Lys Ala Tyr	
255 260 265 270	
gac aag gct gca atc aac act aat ggt aga gaa gca gtc acg aac ttc	1104
Asp Lys Ala Ala Ile Asn Thr Asn Gly Arg Glu Ala Val Thr Asn Phe	
275 280 285	
gag atg agt tca tac caa aat gag att aac tct gag agc aat aac tct	1152
Glu Met Ser Ser Tyr Gln Asn Glu Ile Asn Ser Glu Ser Asn Asn Ser	
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gag att gac ctc aac ttg gga atc tct tta tcg acc ggt aat gcg cca	1200
Glu Ile Asp Leu Asn Leu Gly Ile Ser Leu Ser Thr Gly Asn Ala Pro	
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Gln Arg Gly Val Ser Leu Arg Ile Asp Asn Glu Tyr Met Gly Lys Pro	
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Val Asn Thr Pro Leu Pro Tyr Gly Ser Ser Asp His Arg Leu Tyr Trp	
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Asn Gly Ala Cys Pro Ser Tyr Asn Asn Pro Ala Glu Gly Arg Ala Thr	
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Glu Lys Arg Ser Glu Ala Glu Gly Met Met Ser Asn Trp Gly Trp Gln	
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Arg Pro Gly Gln Thr Ser Ala Val Arg Pro Gln Pro Pro Gly Pro Gln	
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Pro Pro Pro Leu Phe Ser Val Ala Ala Ala Ser Gly Phe Ser His	
415 420 425 430	
ttc cgg cca caa cct ccc aat gac aat gca aca cgt ggt tac ttt tat	1584
Phe Arg Pro Gln Pro Pro Asn Asp Asn Ala Thr Arg Gly Tyr Phe Tyr	
435 440 445	
cca cac cct taacttgtaa ggggacatat gagagttttt ttaccatctc	1633
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 Asp Gly Asp Glu Asp Ser Cys Ser Thr Arg Ala Phe Thr Leu Ser Phe
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 Asp Ile Leu Lys Val Gly Ser Ser Ser Gly Gly Asp Glu Ser Pro Ala
 65 70 75 80
 Ala Ser Ala Ser Val Thr Lys Glu Phe Phe Pro Val Ser Gly Asp Cys
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 Gly His Leu Arg Asp Val Glu Gly Ser Ser Ser Ser Arg Asn Trp Ile
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 Asp Leu Ser Phe Asp Arg Ile Gly Asp Gly Glu Thr Lys Leu Val Thr
 115 120 125
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 Arg Gly Pro Arg Ser Arg Ser Ser Gln Tyr Arg Gly Val Thr Phe Tyr
 145 150 155 160
 Arg Arg Thr Gly Arg Trp Glu Ser His Ile Trp Asp Cys Gly Lys Gln
 165 170 175
 Val Tyr Leu Gly Gly Phe Asp Thr Ala His Ala Ala Ala Arg Ala Tyr
 180 185 190
 Asp Arg Ala Ala Ile Lys Phe Arg Gly Val Asp Ala Asp Ile Asn Phe
 195 200 205
 Thr Leu Gly Asp Tyr Glu Glu Asp Met Lys Gln Val Gln Asn Leu Ser
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 Asp Leu Asn Leu Gly Ile Ser Leu Ser Thr Gly Asn Ala Pro Lys Gln
 305 310 315 320
 Asn Gly Arg Leu Phe His Phe Pro Ser Asn Thr Tyr Glu Thr Gln Arg
 325 330 335
 Gly Val Ser Leu Arg Ile Asp Asn Glu Tyr Met Gly Lys Pro Val Asn
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 Thr Pro Leu Pro Tyr Gly Ser Ser Asp His Arg Leu Tyr Trp Asn Gly
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 Ala Cys Pro Ser Tyr Asn Asn Pro Ala Glu Gly Arg Ala Thr Glu Lys
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 Arg Ser Glu Ala Glu Gly Met Met Ser Asn Trp Gly Trp Gln Arg Pro
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Ser	Thr	Ser	Glu	Ser	Phe	Ser	Ala	Thr	Thr	Ala	Lys	Lys	Leu	Ser	Pro	
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cct	ccc	gcg	gcg	gcg	tta	cgc	ctc	tac	cgg	atg	gga	agc	ggc	ggg	agc	209
Pro	Pro	Ala	Ala	Ala	Leu	Arg	Leu	Tyr	Arg	Met	Gly	Ser	Gly	Gly	Ser	
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Ser	Val	Val	Leu	Asp	Pro	Glu	Asn	Gly	Leu	Glu	Thr	Glu	Ser	Arg	Lys	
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cta	cca	tct	tca	aaa	tac	aaa	ggg	gtt	gtt	cct	cag	cct	aac	gga	aga	305
Leu	Pro	Ser	Ser	Lys	Tyr	Lys	Gly	Val	Val	Pro	Gln	Pro	Asn	Gly	Arg	
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Trp	Gly	Ala	Gln	Ile	Tyr	Glu	Lys	His	Gln	Arg	Val	Trp	Leu	Gly	Thr	
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Phe	Asn	Glu	Gln	Glu	Glu	Ala	Ala	Arg	Ser	Tyr	Asp	Ile	Ala	Ala	Cys	
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Arg	Phe	Arg	Gly	Arg	Asp	Ala	Val	Val	Asn	Phe	Lys	Asn	Val	Leu	Glu	
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Asp	Gly	Asp	Leu	Ala	Phe	Leu	Glu	Ala	His	Ser	Lys	Ala	Glu	Ile	Val	
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Lys	Arg	Gln	Leu	Phe	Leu	Ser	Val	Asp	Ala	Asn	Gly	Lys	Arg	Asn	Gly	
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tcg	agt	act	act	caa	aac	gac	aaa	gtt	tta	aag	acg	tgt	gaa	gtt	ctt	641
Ser	Ser	Thr	Thr	Gln	Asn	Asp	Lys	Val	Leu	Lys	Thr	Cys	Glu	Val	Leu	
			175					180					185			
ttc	gag	aag	gct	gtt	aca	cct	agc	gac	gtt	ggg	aag	cta	aac	cgt	ctc	689
Phe	Glu	Lys	Ala	Val	Thr	Pro	Ser	Asp	Val	Gly	Lys	Leu	Asn	Arg	Leu	
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gtg	ata	cct	aaa	caa	cac	gcc	gag	aaa	cac	ttt						

Leu Arg Leu Tyr Arg Met Gly Ser Gly Gly Ser Ser Val Val Leu Asp
35 40 45

Pro	Glu	Asn	Gly	Leu	Glu	Thr	Glu	Ser	Arg	Lys	Leu	Pro	Ser	Ser	Lys
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Glu	Ala	Ala	Arg	Ser	Tyr	Asp	Ile	Ala	Ala	Cys	Arg	Phe	Arg	Gly	Arg
		100						105				110			
Asp	Ala	Val	Val	Asn	Phe	Lys	Asn	Val	Leu	Glu	Asp	Gly	Asp	Leu	Ala
		115				120						125			
Phe	Leu	Glu	Ala	His	Ser	Lys	Ala	Glu	Ile	Val	Asp	Met	Leu	Arg	Lys
130						135				140					
His	Thr	Tyr	Ala	Asp	Glu	Leu	Glu	Gln	Asn	Asn	Lys	Arg	Gln	Leu	Phe
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Leu	Ser	Val	Asp	Ala	Asn	Gly	Lys	Arg	Asn	Gly	Ser	Ser	Thr	Thr	Gln
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Asn	Asp	Lys	Val	Leu	Lys	Thr	Cys	Glu	Val	Leu	Phe	Glu	Lys	Ala	Val
		180						185				190			
Thr	Pro	Ser	Asp	Val	Gly	Lys	Leu	Asn	Arg	Leu	Val	Ile	Pro	Lys	Gln
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 Thr Ala Val Phe Tyr Leu Arg Gly Pro Ser Ala Arg Leu Asn Phe Pro
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Gln Asn Ser Asn Ile Ser Phe Glu Asn Met Cys Phe Met Glu Glu Lys	
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Val	Tyr	Leu	Asp	Ser	Gly	Ala	Val	Val	Thr	Gly	Ser	Cys	Gly	Gln	Met					
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654160"6T66660

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Asp Lys Ser Asp Gln His Gln Pro Asp Gln Asp Gln Pro Arg Arg Arg
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Ile Arg Asp Pro Lys Lys Ala Ala Arg Val Trp Leu Gly Thr Phe Glu
55 60 65

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Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Arg Ala Ala Leu Lys Phe
70 75 80 85

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Lys Gly Thr Lys Ala Lys Leu Asn Phe Pro Glu Arg Val Gln Gly Pro
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Thr Thr Thr Thr Thr Ile Ser His Ala Pro Arg Gly Val Ser Glu Ser
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200 205 210

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Val Thr Asn Phe Lys Asp Val Lys Met Asp Glu Asp Glu Val Asp Phe
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aaa act gat ggc aag ata gct gtg tca gct tct cct gct gtt cct agg 757
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180 185 190

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Trp Asp Phe
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Phe Cys Leu Arg Gly Gly Asp Ala Asn Phe Asn Phe Pro Asn Asn Pro
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 Glu Glu Ser Gly Leu Val Pro Gly Ser Glu Ile Arg Pro Glu Ser Pro
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Ile Ala Phe Gly Ile Leu Lys Arg Asp Asp Asp Leu Val Pro Pro Pro
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Pro Pro Pro Pro His Lys Glu Thr Gly Asp Leu Phe Pro Val Val Ala
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 85 90 95

Asn Leu Ser Ser Leu Gln Arg Asn Thr Gln Lys Met Val Lys Lys Ser
 100 105 110

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Leu Pro Ala Pro Ile Ser Tyr Gly Ser Asp Leu His Ser Phe Ser His																
45 50 55 60																
cat ctt agt cct aaa ccg gtc tca atg aaa caa acc ggt act tcc gcg																604
His Leu Ser Pro Lys Pro Val Ser Met Lys Gln Thr Gly Thr Ser Ala																
65 70 75																
gct aaa ccg acg aag cta tac aga gga gtg aga caa cgt cac tgg gga																652
Ala Lys Pro Thr Lys Leu Tyr Arg Gly Val Arg Gln Arg His Trp Gly																
80 85 90																
aaa tgg gtg gct gag att cgt tta ccg agg aat cga act cga ctt tgg																700
Lys Trp Val Ala Glu Ile Arg Leu Pro Arg Asn Arg Thr Arg Leu Trp																
95 100 105																
ctc gga aca ttc gac acg gcg gag gaa gct gct tta gct tat gac aag																748
Leu Gly Thr Phe Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Lys																
110 115 120																
gcg gcg tat aag ctc cga gga gat ttt gcg cgg ctt aat ttc cct gat																796
Ala Ala Tyr Lys Leu Arg Gly Asp Phe Ala Arg Leu Asn Phe Pro Asp																
125 130 135 140																
ctc cgt cat aac gac gag tat caa cct ctt caa tca tca gtc gac gct																844
Leu Arg His Asn Asp Glu Tyr Gln Pro Leu Gln Ser Ser Val Asp Ala																
145 150 155																
aag ctt gaa gct att tgt caa aac tta gct gag acg acg cag aaa cag																892
Lys Leu Glu Ala Ile Cys Gln Asn Leu Ala Glu Thr Thr Gln Lys Gln																
160 165 170																
gtg aga tca acg aag aag tct tct tct cgg aaa cgt tca tca acc gtc																940
Val Arg Ser Thr Lys Lys Ser Ser Arg Lys Arg Ser Ser Thr Val																
175 180 185																
gca gtg aaa cta ccg gag gag gac tac tct agc gcc gga tct tcg ccg																988
Ala Val Lys Leu Pro Glu Glu Asp Tyr Ser Ser Ala Gly Ser Ser Pro																
190 195 200																

ctg tta acg gag agt tat gga tct ggt gga tct tct tcg ccg ttg tcg 1036
 Leu Leu Thr Glu Ser Tyr Gly Ser Gly Gly Ser Ser Ser Pro Leu Ser
 205 210 215 220

gag ctg acg ttt ggt gat acg gag gag gag att cag ccg ccg tgg aac 1084
 Glu Leu Thr Phe Gly Asp Thr Glu Glu Glu Ile Gln Pro Pro Trp Asn
 225 230 235

gag aac gcg ttg gag aag tat ccg tcg tac gag atc gat tgg gat tcg 1132
 Glu Asn Ala Leu Glu Lys Tyr Pro Ser Tyr Glu Ile Asp Trp Asp Ser
 240 245 250

att ctt cag tgt tcg agt ctt gta aat tagatgttgc cataggggta 1179
 Ile Leu Gln Cys Ser Ser Leu Val Asn
 255 260

ttttagggac tttagagctc tctgcgatgg agtttttgggt cattgcagag attttattat 1239

tattaagggg gtttggtatg ttaatatcaa ataagtttat ctactttgat gttaattagt 1299

gttaatctct gcgtcgggcc aagctgtttt tttttggcat gcttcgaccg tgtgagattt 1359

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aaaaaaaaa a 1430

<210> 26

<211> 261

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<213> Arabidopsis thaliana

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<223> G974

<400> 26

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Ser Pro Ser Asn Asp Ser Ser Ala Phe Ala Phe Ser Leu Pro Ala Pro
 35 40 45

Ile Ser Tyr Gly Ser Asp Leu His Ser Phe Ser His His Leu Ser Pro
 50 55 60

Lys Pro Val Ser Met Lys Gln Thr Gly Thr Ser Ala Ala Lys Pro Thr
 65 70 75 80

Lys Leu Tyr Arg Gly Val Arg Gln Arg His Trp Gly Lys Trp Val Ala
 85 90 95

Glu Ile Arg Leu Pro Arg Asn Arg Thr Arg Leu Trp Leu Gly Thr Phe
 100 105 110

Asp Thr Ala Glu Glu Ala Ala Leu Ala Tyr Asp Lys Ala Ala Tyr Lys
115 120 125

Leu Arg Gly Asp Phe Ala Arg Leu Asn Phe Pro Asp Leu Arg His Asn
130 135 140

Asp Glu Tyr Gln Pro Leu Gln Ser Ser Val Asp Ala Lys Leu Glu Ala
145 150 155 160

Ile Cys Gln Asn Leu Ala Glu Thr Thr Gln Lys Gln Val Arg Ser Thr
165 170 175

Lys Lys Ser Ser Ser Arg Lys Arg Ser Ser Thr Val Ala Val Lys Leu
180 185 190

Pro Glu Glu Asp Tyr Ser Ser Ala Gly Ser Ser Pro Leu Leu Thr Glu
195 200 205

Ser Tyr Gly Ser Gly Gly Ser Ser Ser Pro Leu Ser Glu Leu Thr Phe
210 215 220

Gly Asp Thr Glu Glu Glu Ile Gln Pro Pro Trp Asn Glu Asn Ala Leu
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Glu Lys Tyr Pro Ser Tyr Glu Ile Asp Trp Asp Ser Ile Leu Gln Cys
245 250 255

Ser Ser Leu Val Asn
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<210> 27
<211> 795
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (58)..(654)
<223> G975

<220>
<223> "n" at various positions throughout the sequence
may be A, T, C, G, other or unknown

<220>
<223> Xaa at amino acid position 90 is either a Serine
or not present

<400> 27
attactcatc atcaagttcc tacttttctct ctgacaaaca tcacagagta agtaaga 57

atg gta cag acg aag aag ttc aga ggt gtc agg caa cgc cat tgg ggt 105
Met Val Gln Thr Lys Lys Phe Arg Gly Val Arg Gln Arg His Trp Gly
1 5 10 15

tct tgg gtc gct gag att cgt cat cct ctc ttg aaa cgg agg att tgg 153
Ser Trp Val Ala Glu Ile Arg His Pro Leu Leu Lys Arg Arg Ile Trp
20 25 30

cta ggg acg ttc gag acc gca gag gag gca gca aga gca tac gac gag 201
Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu
35 40 45

gcc gcc gtt tta atg agc ggc cgc aac gcc aaa acc aac ttt ccc ctc 249
Ala Ala Val Leu Met Ser Gly Arg Asn Ala Lys Thr Asn Phe Pro Leu
50 55 60

aac aac aac aac acc gga gaa act tcc gag ggc aaa acc gat att tca 297
Asn Asn Asn Asn Thr Gly Glu Thr Ser Glu Gly Lys Thr Asp Ile Ser
65 70 75 80

gct tgc tcc aca atg tca tcc tca aca tma tct tca tgc ctc tct tcc 345
Ala Ser Ser Thr Met Ser Ser Ser Thr Xaa Ser Ser Ser Leu Ser Ser
85 90 95

atc ctc agc gcc aaa ctg agg aaa tgc tgc aag tct cct tcc cca tcc 393
Ile Leu Ser Ala Lys Leu Arg Lys Cys Cys Lys Ser Pro Ser Pro Ser
100 105 110

ctc acc tgc ctc cgt ctt gac aca gcc agc tcc cat atc ggc gtc tgg 441
Leu Thr Cys Leu Arg Leu Asp Thr Ala Ser Ser His Ile Gly Val Trp
115 120 125

cag aaa cgg gcc ggt tca aag tct gac tcc agc tgg gtc atg acg gtg 489
Gln Lys Arg Ala Gly Ser Lys Ser Asp Ser Ser Trp Val Met Thr Val
130 135 140

gag cta ggt ccc gca agc tcc tcc caa gag act act agt aaa gct tca 537
Glu Leu Gly Pro Ala Ser Ser Ser Gln Glu Thr Thr Ser Lys Ala Ser
145 150 155 160

caa gac gct att ctt gct ccg acc act gaa gtt gaa att ggt ggc agc 585
Gln Asp Ala Ile Leu Ala Pro Thr Thr Glu Val Glu Ile Gly Gly Ser
165 170 175

aga gaa gaa gta ttg gat gag gaa gaa aag gtt gct ttg caa atg ata 633
Arg Glu Glu Val Leu Asp Glu Glu Glu Lys Val Ala Leu Gln Met Ile
180 185 190

gag gag ctt ctc aat aca aac taaatcttat ttgcttatat atatgtacct 684
Glu Glu Leu Leu Asn Thr Asn
195

atcttcattg ctgatttaca gccaaaataa tcaattatac cgtgtatttt atagatgttt 744

tatattaataa gggtgttaga tatananana nnnnnnnnnn ananannna a 795

<210> 28

<211> 199

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G975

<220>

<223> Xaa at amino acid position 90 is either a Serine
or not present

<400> 28

Met Val Gln Thr Lys Lys Phe Arg Gly Val Arg Gln Arg His Trp Gly
1 5 10 15Ser Trp Val Ala Glu Ile Arg His Pro Leu Leu Lys Arg Arg Ile Trp
20 25 30Leu Gly Thr Phe Glu Thr Ala Glu Glu Ala Ala Arg Ala Tyr Asp Glu
35 40 45Ala Ala Val Leu Met Ser Gly Arg Asn Ala Lys Thr Asn Phe Pro Leu
50 55 60Asn Asn Asn Asn Thr Gly Glu Thr Ser Glu Gly Lys Thr Asp Ile Ser
65 70 75 80Ala Ser Ser Thr Met Ser Ser Ser Thr Xaa Ser Ser Ser Leu Ser Ser
85 90 95Ile Leu Ser Ala Lys Leu Arg Lys Cys Cys Lys Ser Pro Ser Pro Ser
100 105 110Leu Thr Cys Leu Arg Leu Asp Thr Ala Ser Ser His Ile Gly Val Trp
115 120 125Gln Lys Arg Ala Gly Ser Lys Ser Asp Ser Ser Trp Val Met Thr Val
130 135 140Glu Leu Gly Pro Ala Ser Ser Ser Gln Glu Thr Thr Ser Lys Ala Ser
145 150 155 160Gln Asp Ala Ile Leu Ala Pro Thr Thr Glu Val Glu Ile Gly Gly Ser
165 170 175Arg Glu Glu Val Leu Asp Glu Glu Glu Lys Val Ala Leu Gln Met Ile
180 185 190Glu Glu Leu Leu Asn Thr Asn
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<210> 29

<211> 966

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (72)..(815)

<223> G976

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<220>

<223> "n" at various positions throughout the sequence
may be A, T, C, G, other or unknown

<220>

<223> Xaa at amino acid position 77 may be various or
unknown

<400> 29

ggtcttatat ataacaaata aacacataag ttgacatata tactatatac aagtatatta 60

attatacata t atg gct gac cct aac aat cct atc act gaa cct aaa gct 110
Met Ala Asp Pro Asn Asn Pro Ile Thr Glu Pro Lys Ala
1 5 10

ata atc caa tct tct act tca tgc tca gtt act att gtg cca gtt ccc 158
Ile Ile Gln Ser Ser Thr Ser Ser Val Thr Ile Val Pro Val Pro
15 20 25

acg tgc ggt gac agc ctc tct gac tct gcc acg tgt gaa aac cct tgt 206
Thr Cys Gly Asp Ser Leu Ser Asp Ser Ala Thr Cys Glu Asn Pro Cys
30 35 40 45

cca ctt gat act atc act act act act act act gtt tgt ttt gcg gct 254
Pro Leu Asp Thr Ile Thr Thr Thr Thr Thr Val Cys Phe Ala Ala
50 55 60

cct tct tct act gca agt ggt aat gat att aat act tta atg gcc nct 302
Pro Ser Ser Thr Ala Ser Gly Asn Asp Ile Asn Thr Leu Met Ala Xaa
65 70 75

gac acc gac atc tct cgc cgg aaa aag aat ccg gtt tat cgg gga att 350
Asp Thr Asp Ile Ser Arg Arg Lys Lys Asn Pro Val Tyr Arg Gly Ile
80 85 90

cgt tgt cgg agt gga aaa tgg gtg tct gaa atc cga gag cct aaa aag 398
Arg Cys Arg Ser Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys
95 100 105

act aca cgt gtc tgg ctt ggg act tat ccg acg ccg gag atg gct gct 446
Thr Thr Arg Val Trp Leu Gly Thr Tyr Pro Thr Pro Glu Met Ala Ala
110 115 120 125

gcc gca tat gac gtg gcg gcg tta gct ctt aaa ggt gga gac act ctc 494
Ala Ala Tyr Asp Val Ala Ala Leu Ala Leu Lys Gly Gly Asp Thr Leu
130 135 140

ttg aac ttc ccg gat tcc ctg gga tct tac ccc att ccc ata tct tct 542
Leu Asn Phe Pro Asp Ser Leu Gly Ser Tyr Pro Ile Pro Ile Ser Ser
145 150 155

tcc gca gct cat atc aga tgc gct gca gct gcg gct gct gcg act agg 590
Ser Ala Ala His Ile Arg Cys Ala Ala Ala Ala Ala Ala Thr Arg
160 165 170

ggt gcg gct gga gcg gcc gtg aag gta ggt caa aag aag gaa gat aaa 638
Gly Ala Ala Gly Ala Ala Val Lys Val Gly Gln Lys Lys Glu Asp Lys
175 180 185

554150 "51545550

gtt tat gat acg gcg gaa tct tca act atg ggg ttt gtg gat gaa gaa 686
 Val Tyr Asp Thr Ala Glu Ser Ser Thr Met Gly Phe Val Asp Glu Glu
 190 195 200 205

gag cta ttg aac atg cct ggt ttg cta gcg gat atg gcc aaa ggg atg 734
 Glu Leu Leu Asn Met Pro Gly Leu Leu Ala Asp Met Ala Lys Gly Met
 210 215 220

atg gtg gct cca ccg tgg atg gga tct cca ccg tca gat gat tcg cca 782
 Met Val Ala Pro Pro Trp Met Gly Ser Pro Pro Ser Asp Asp Ser Pro
 225 230 235

gag aat tct gat gga gag agc ttg tgg agc tat tgatcgattg aaagcagttt 835
 Glu Asn Ser Asp Gly Glu Ser Leu Trp Ser Tyr
 240 245

aatatctttt ttggatcctt tgttcacggt tatgctagtc atctttgttt ctttatccta 895

tgattgtag agatgatttg ttaaataatat aatcgtaatg attttcactt ttttttattc 955

aaaaaaaaa a 966

<210> 30

<211> 248

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G976

<220>

<223> Xaa at amino acid position 77 may be various or
 unknown

<400> 30

Met Ala Asp Pro Asn Asn Pro Ile Thr Glu Pro Lys Ala Ile Ile Gln
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Ser Ser Thr Ser Ser Ser Val Thr Ile Val Pro Val Pro Thr Cys Gly
 20 25 30

Asp Ser Leu Ser Asp Ser Ala Thr Cys Glu Asn Pro Cys Pro Leu Asp
 35 40 45

Thr Ile Thr Thr Thr Thr Thr Thr Val Cys Phe Ala Ala Pro Ser Ser
 50 55 60

Thr Ala Ser Gly Asn Asp Ile Asn Thr Leu Met Ala Xaa Asp Thr Asp
 65 70 75 80

Ile Ser Arg Arg Lys Lys Asn Pro Val Tyr Arg Gly Ile Arg Cys Arg
 85 90 95

Ser Gly Lys Trp Val Ser Glu Ile Arg Glu Pro Lys Lys Thr Thr Arg
 100 105 110

Val Trp Leu Gly Thr Tyr Pro Thr Pro Glu Met Ala Ala Ala Ala Tyr
 115 120 125

Asp Val Ala Ala Leu Ala Leu Lys Gly Gly Asp Thr Leu Leu Asn Phe
 130 135 140

Pro Asp Ser Leu Gly Ser Tyr Pro Ile Pro Ile Ser Ser Ser Ala Ala
 145 150 155 160

His Ile Arg Cys Ala Ala Ala Ala Ala Ala Thr Arg Gly Ala Ala
 165 170 175

Gly Ala Ala Val Lys Val Gly Gln Lys Lys Glu Asp Lys Val Tyr Asp
 180 185 190

Thr Ala Glu Ser Ser Thr Met Gly Phe Val Asp Glu Glu Glu Leu Leu
 195 200 205

Asn Met Pro Gly Leu Leu Ala Asp Met Ala Lys Gly Met Met Val Ala
 210 215 220

Pro Pro Trp Met Gly Ser Pro Pro Ser Asp Asp Ser Pro Glu Asn Ser
 225 230 235 240

Asp Gly Glu Ser Leu Trp Ser Tyr
 245

<210> 31
 <211> 833
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (46)..(588)
 <223> G977

<220>
 <223> "n" at various positions throughout the sequence
 may be A, T, C, G, other or unknown

<400> 31
 caccaaaactc acctgaaacc ctatttccat ttaccattca cacta atg gca cga cca 57
 Met Ala Arg Pro
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caa caa cgc ttt cga ggc gtt aga cag agg cat tgg ggc tct tgg gtc 105
 Gln Gln Arg Phe Arg Gly Val Arg Gln Arg His Trp Gly Ser Trp Val
 5 10 15 20

tcc gaa att cgt cac cct ctc ttg aaa aca aga atc tgg cta ggg acg 153
 Ser Glu Ile Arg His Pro Leu Leu Lys Thr Arg Ile Trp Leu Gly Thr
 25 30 35

ttt gag aca gcg gag gat gca gca agg gcc tac gac gag gcg gct agg 201
 Phe Glu Thr Ala Glu Asp Ala Ala Arg Ala Tyr Asp Glu Ala Ala Arg
 40 45 50


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<210> 32
<211> 181
<212> PRT
<213> Arabidopsis thaliana

<220>
<223> G977

<400> 32
Met Ala Arg Pro Gln Gln Arg Phe Arg Gly Val Arg Gln Arg His Trp
  1                   5                10                  15
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<210> 33
<211> 1530
<212> DNA
<213> Arabidopsis thaliana
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<220>
<223> "n" at various positions throughout the sequence
may be A, T, C, G, other or unknown
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<400> 33
cctctgagga atcaaatcac tcacactcca aaaaaaaatc taaactttct cagagttaa 59
atg aag aag cgc tta acc act tcc act tgt tct tct tct cca tct tcc 107
Met Lys Lys Arg Leu Thr Thr Ser Thr Cys Ser Ser Ser Pro Ser Ser
  1             5             10             15

tct gtt tct tct tct act act act tcc tct cct att cag tcg gag gct 155
Ser Val Ser Ser Ser Thr Thr Thr Ser Ser Pro Ile Gln Ser Glu Ala
      20             25             30

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cca	agg	cct	aaa	cga	gcc	aaa	agg	gct	aag	aaa	tct	tct	cct	tct	ggc	203
Pro	Arg	Pro	Lys	Arg	Ala	Lys	Arg	Ala	Lys	Lys	Ser	Ser	Pro	Ser	Gly	
		35					40					45				
gat	aaa	tct	cat	aac	ccg	aca	agc	cct	gct	tct	acc	cga	cgc	agc	tct	251
Asp	Lys	Ser	His	Asn	Pro	Thr	Ser	Pro	Ala	Ser	Thr	Arg	Arg	Ser	Ser	
	50					55					60					
atc	tac	aga	gga	gtc	act	aga	cat	aga	tgg	act	ggg	aga	ttc	gag	gct	299
Ile	Tyr	Arg	Gly	Val	Thr	Arg	His	Arg	Trp	Thr	Gly	Arg	Phe	Glu	Ala	
	65				70				75						80	
cat	ctt	tgg	gac	aaa	agc	tct	tgg	aat	tgc	att	cag	aac	aag	aaa	ggc	347
His	Leu	Trp	Asp	Lys	Ser	Ser	Trp	Asn	Ser	Ile	Gln	Asn	Lys	Lys	Gly	
				85				90						95		
aaa	caa	gtt	tat	ctg	gga	gca	tat	gac	agt	gaa	gaa	gca	gca	gca	cat	395
Lys	Gln	Val	Tyr	Leu	Gly	Ala	Tyr	Asp	Ser	Glu	Glu	Ala	Ala	Ala	His	
		100						105					110			
acg	tac	gat	ctg	gct	gct	ctc	aag	tac	tgg	gga	ccc	gac	acc	atc	ttg	443
Thr	Tyr	Asp	Leu	Ala	Ala	Leu	Lys	Tyr	Trp	Gly	Pro	Asp	Thr	Ile	Leu	
		115					120					125				
aat	ttt	ccg	gca	gag	acg	tac	aca	aag	gaa	ttg	gaa	gaa	atg	cag	aga	491
Asn	Phe	Pro	Ala	Glu	Thr	Tyr	Thr	Lys	Glu	Leu	Glu	Glu	Met	Gln	Arg	
	130					135					140					
gtg	aca	aag	gaa	gaa	tat	ttg	gct	tct	ctc	cgc	cgc	cag	agc	agt	ggc	539
Val	Thr	Lys	Glu	Glu	Tyr	Leu	Ala	Ser	Leu	Arg	Arg	Gln	Ser	Ser	Gly	
	145				150				155						160	
ttc	tcc	aga	ggc	gtc	tct	aaa	tat	cgc	ggc	gtc	gct	agg	cat	cac	cac	587
Phe	Ser	Arg	Gly	Val	Ser	Lys	Tyr	Arg	Gly	Val	Ala	Arg	His	His	His	
			165					170						175		
aac	gga	aga	tgg	gag	gct	cgg	atc	gga	aga	gtg	ttt	ggg	aac	aag	tac	635
Asn	Gly	Arg	Trp	Glu	Ala	Arg	Ile	Gly	Arg	Val	Phe	Gly	Asn	Lys	Tyr	
		180					185					190				
ttg	tac	ctc	ggc	acc	tat	aat	acg	cag	gag	gaa	gct	gct	gca	gca	tat	683
Leu	Tyr	Leu	Gly	Thr	Tyr	Asn	Thr	Gln	Glu	Glu	Ala	Ala	Ala	Ala	Tyr	
		195				200						205				
gac	atg	gct	gcg	att	gag	tat	cga	ggc	gca	aac	gcg	gtt	act	aat	ttc	731
Asp	Met	Ala	Ala	Ile	Glu	Tyr	Arg	Gly	Ala	Asn	Ala	Val	Thr	Asn	Phe	
	210					215					220					
gac	att	agt	aat	tac	att	gac	cgg	tta	aag	aag	aaa	ggc	gtt	ttc	ccg	779
Asp	Ile	Ser	Asn	Tyr	Ile	Asp	Arg	Leu	Lys	Lys	Lys	Gly	Val	Phe	Pro	
	225				230				235						240	
ttc	cct	gtg	aac	caa	gct	aac	cat	caa	gag	ggc	att	ctt	gtt	gaa	gcc	827
Phe	Pro	Val	Asn	Gln	Ala	Asn	His	Gln	Glu	Gly	Ile	Leu	Val	Glu	Ala	
			245					250						255		

aaa caa gaa gtt gaa acg aga gaa gcg aag gaa gag cct aga gaa gaa 875
 Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu
 260 265 270

gtg aaa caa cag tac gtg gaa gaa cca ccg caa gaa gaa gaa gag aag 923
 Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Glu Lys
 275 280 285

gaa gaa gag aaa gca gag caa caa gaa gca gag att gta gga tat tca 971
 Glu Glu Glu Lys Ala Glu Gln Gln Glu Ala Glu Ile Val Gly Tyr Ser
 290 295 300

gaa gaa gca gca gtg gtc aat tgc tgc ata gac tct tca acc ata atg 1019
 Glu Glu Ala Ala Val Val Asn Cys Cys Ile Asp Ser Ser Thr Ile Met
 305 310 315 320

gaa atg gat cgt tgt ggg gac aac aat gag ctg gct tgg aac ttc tgt 1067
 Glu Met Asp Arg Cys Gly Asp Asn Asn Glu Leu Ala Trp Asn Phe Cys
 325 330 335

atg atg gat aca ggg ttt tct ccg ttt ttg act gat cag aat ctc gcg 1115
 Met Met Asp Thr Gly Phe Ser Pro Phe Leu Thr Asp Gln Asn Leu Ala
 340 345 350

aat gag aat ccc ata gag tat ccg gag cta ttc aat gag tta gca ttt 1163
 Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe
 355 360 365

gag gac aac atc gac ttc atg ttc gat gat ggg aag cac gag tgc ttg 1211
 Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu
 370 375 380

aac ttg gaa aat ctg gat tgt tgc gtg gtg gga aga gag agc cca ccc 1259
 Asn Leu Glu Asn Leu Asp Cys Cys Val Val Gly Arg Glu Ser Pro Pro
 385 390 395 400

tct tct tct tca cca ttg tct tgc tta tct act gac tct gct tca tca 1307
 Ser Ser Ser Ser Pro Leu Ser Cys Leu Ser Thr Asp Ser Ala Ser Ser
 405 410 415

aca aca aca aca aca acc tcg gtt tct tgt aac tat ttg gtc 1349
 Thr Thr Thr Thr Thr Thr Ser Val Ser Cys Asn Tyr Leu Val
 420 425 430

tgagagagag agctttgcct tctagtttga atttctatatt cttccgcttc ttcttctttt 1409
 ttttctttttg ttgggttctg cttagggttt gtatttcagt ttcagggtt gttcgttggg 1469
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 a 1530

<210> 34

<211> 430

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G979

<400> 34

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Met Lys Lys Arg Leu Thr Thr Ser Thr Cys Ser Ser Ser Pro Ser Ser
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Ser Val Ser Ser Ser Thr Thr Thr Ser Ser Pro Ile Gln Ser Glu Ala
      20              25              30

Pro Arg Pro Lys Arg Ala Lys Arg Ala Lys Lys Ser Ser Pro Ser Gly
      35              40              45

Asp Lys Ser His Asn Pro Thr Ser Pro Ala Ser Thr Arg Arg Ser Ser
 50              55              60

Ile Tyr Arg Gly Val Thr Arg His Arg Trp Thr Gly Arg Phe Glu Ala
 65              70              75              80

His Leu Trp Asp Lys Ser Ser Trp Asn Ser Ile Gln Asn Lys Lys Gly
      85              90

Lys Gln Val Tyr Leu Gly Ala Tyr Asp Ser Glu Glu Ala Ala Ala His
      100              105              110

Thr Tyr Asp Leu Ala Ala Leu Lys Tyr Trp Gly Pro Asp Thr Ile Leu
 115              120              125

Asn Phe Pro Ala Glu Thr Tyr Thr Lys Glu Leu Glu Glu Met Gln Arg
 130              135              140

Val Thr Lys Glu Glu Tyr Leu Ala Ser Leu Arg Arg Gln Ser Ser Gly
 145              150              155              160

Phe Ser Arg Gly Val Ser Lys Tyr Arg Gly Val Ala Arg His His His
      165              170              175

Asn Gly Arg Trp Glu Ala Arg Ile Gly Arg Val Phe Gly Asn Lys Tyr
      180              185              190

Leu Tyr Leu Gly Thr Tyr Asn Thr Gln Glu Glu Ala Ala Ala Tyr
 195              200              205

Asp Met Ala Ala Ile Glu Tyr Arg Gly Ala Asn Ala Val Thr Asn Phe
 210              215              220

Asp Ile Ser Asn Tyr Ile Asp Arg Leu Lys Lys Lys Gly Val Phe Pro
 225              230              235              240

Phe Pro Val Asn Gln Ala Asn His Gln Glu Gly Ile Leu Val Glu Ala
      245              250              255

Lys Gln Glu Val Glu Thr Arg Glu Ala Lys Glu Glu Pro Arg Glu Glu
      260              265              270

Val Lys Gln Gln Tyr Val Glu Glu Pro Pro Gln Glu Glu Glu Lys
      275              280              285

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Glu Glu Glu Lys Ala Glu Gln Gln Glu Ala Glu Ile Val Gly Tyr Ser
290 295 300

Glu Glu Ala Ala Val Val Asn Cys Cys Ile Asp Ser Ser Thr Ile Met
305 310 315 320

Glu Met Asp Arg Cys Gly Asp Asn Asn Glu Leu Ala Trp Asn Phe Cys
325 330 335

Met Met Asp Thr Gly Phe Ser Pro Phe Leu Thr Asp Gln Asn Leu Ala
340 345 350

Asn Glu Asn Pro Ile Glu Tyr Pro Glu Leu Phe Asn Glu Leu Ala Phe
355 360 365

Glu Asp Asn Ile Asp Phe Met Phe Asp Asp Gly Lys His Glu Cys Leu
370 375 380

Asn Leu Glu Asn Leu Asp Cys Cys Val Val Gly Arg Glu Ser Pro Pro
385 390 395 400

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<223> G993

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Leu Ser Ile Ser Thr Thr Pro Lys Pro Thr Thr Thr Thr Glu Lys Lys
20 25 30

ctc tct tct ccg ccg gcg acg tcg atg cgt ctc tac aga atg gga agc 146
Leu Ser Ser Pro Pro Ala Thr Ser Met Arg Leu Tyr Arg Met Gly Ser
35 40 45

ggc gga agc agc gtc gtt ttg gat tca gag aac ggc gtc gag acc gag 194
Gly Gly Ser Ser Val Val Leu Asp Ser Glu Asn Gly Val Glu Thr Glu
50 55 60

tca cgt aag ctt cct tcg tcg aaa tat aaa ggc gtt gtg cct cag cct 242
Ser Arg Lys Leu Pro Ser Ser Lys Tyr Lys Gly Val Val Pro Gln Pro
65 70 75

aac gga aga tgg gga gct cag att tac gag aag cat cag cga gtt tgg	290
Asn Gly Arg Trp Gly Ala Gln Ile Tyr Glu Lys His Gln Arg Val Trp	
80 85 90 95	
ctc ggt act ttc aac gag gaa gaa gaa gct gcg tct tct tac gac atc	338
Leu Gly Thr Phe Asn Glu Glu Glu Glu Ala Ala Ser Ser Tyr Asp Ile	
100 105 110	
gcc gtg agg aga ttc cgc gcc cgc gac gcc gtc act aac ttc aaa tct	386
Ala Val Arg Arg Phe Arg Gly Arg Asp Ala Val Thr Asn Phe Lys Ser	
115 120 125	
caa gtt gat gga aac gac gcc gaa tcg gct ttt ctt gac gct cat tct	434
Gln Val Asp Gly Asn Asp Ala Glu Ser Ala Phe Leu Asp Ala His Ser	
130 135 140	
aaa gct gag atc gtg gat atg ttg agg aaa cac act tac gcc gat gag	482
Lys Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu	
145 150 155	
ttt gag cag agt aga cgg aag ttt gtt aac gcc gac gga aaa cgc tct	530
Phe Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser	
160 165 170 175	
ggg ttg gag acg gcg acg tac gga aac gac gct gtt ttg aga gcg cgt	578
Gly Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg	
180 185 190	
gag gtt ttg ttc gag aag act gtt acg ccg agc gac gtc ggg aag ctg	626
Glu Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu	
195 200 205	
aac cgt tta gtg ata ccg aaa caa cac gcg gag aag cat ttt ccg tta	674
Asn Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu	
210 215 220	
ccg gcg atg acg acg gcg atg ggg atg aat ccg tct ccg acg aaa ggc	722
Pro Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly	
225 230 235	
gtt ttg att aac ttg gaa gat aga aca ggg aaa gtg tgg cgg ttc cgt	770
Val Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg	
240 245 250 255	
tac agt tac tgg aac agc agt caa agt tac gtg ttg acc aag ggc tgg	818
Tyr Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp	
260 265 270	
agc cgg ttc gtt aaa gag aag aat ctt cga gcc ggt gat gtg gtt tgt	866
Ser Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys	
275 280 285	
ttc gag aga tca acc gga cca gac cgg caa ttg tat atc cac tgg aaa	914
Phe Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys	
290 295 300	

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gtc  cgg  tct  agt  ccg  gtt  cag  act  gtg  gtt  agg  cta  ttc  gga  gtc  aac      962
Val  Arg  Ser  Ser  Pro  Val  Gln  Thr  Val  Val  Arg  Leu  Phe  Gly  Val  Asn
      305                      310                      315

att  ttc  aat  gtg  agt  aac  gag  aaa  cca  aac  gac  gtc  gca  gta  gag  tgt      1010
Ile  Phe  Asn  Val  Ser  Asn  Glu  Lys  Pro  Asn  Asp  Val  Ala  Val  Glu  Cys
320                      325                      330                      335

gtt  ggc  aag  aag  aga  tct  cgg  gaa  gat  gat  ttg  ttt  tcg  tta  ggg  tgt      1058
Val  Gly  Lys  Lys  Arg  Ser  Arg  Glu  Asp  Asp  Leu  Phe  Ser  Leu  Gly  Cys
                        340                      345                      350

tcc  aag  aag  cag  gcg  att  atc  aac  atc  ttg  tgacaaattc  tttttttttg      1108
Ser  Lys  Lys  Gln  Ala  Ile  Ile  Asn  Ile  Leu
                        355                      360

gttttttttct  tcaatttggt  tctccttttt  caatatatttg  tattgaaatg  acaagttgta  1168

aattaggaca  agacaagaaa  aaatgacaac  tagacaaaat  agttttttggt  taaaaaaaaa  1228

aaaaaaaaa  a      1239

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                20              25              30

Ser  Ser  Pro  Pro  Ala  Thr  Ser  Met  Arg  Leu  Tyr  Arg  Met  Gly  Ser  Gly
      35              40              45

Gly  Ser  Ser  Val  Val  Leu  Asp  Ser  Glu  Asn  Gly  Val  Glu  Thr  Glu  Ser
      50              55              60

Arg  Lys  Leu  Pro  Ser  Ser  Lys  Tyr  Lys  Gly  Val  Val  Pro  Gln  Pro  Asn
      65              70              75              80

Gly  Arg  Trp  Gly  Ala  Gln  Ile  Tyr  Glu  Lys  His  Gln  Arg  Val  Trp  Leu
                85              90              95

Gly  Thr  Phe  Asn  Glu  Glu  Glu  Glu  Ala  Ala  Ser  Ser  Tyr  Asp  Ile  Ala
      100              105              110

Val  Arg  Arg  Phe  Arg  Gly  Arg  Asp  Ala  Val  Thr  Asn  Phe  Lys  Ser  Gln
      115              120              125

Val  Asp  Gly  Asn  Asp  Ala  Glu  Ser  Ala  Phe  Leu  Asp  Ala  His  Ser  Lys
      130              135              140

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Ala Glu Ile Val Asp Met Leu Arg Lys His Thr Tyr Ala Asp Glu Phe
 145 150 155 160

Glu Gln Ser Arg Arg Lys Phe Val Asn Gly Asp Gly Lys Arg Ser Gly
 165 170 175

Leu Glu Thr Ala Thr Tyr Gly Asn Asp Ala Val Leu Arg Ala Arg Glu
 180 185 190

Val Leu Phe Glu Lys Thr Val Thr Pro Ser Asp Val Gly Lys Leu Asn
 195 200 205

Arg Leu Val Ile Pro Lys Gln His Ala Glu Lys His Phe Pro Leu Pro
 210 215 220

Ala Met Thr Thr Ala Met Gly Met Asn Pro Ser Pro Thr Lys Gly Val
 225 230 235 240

Leu Ile Asn Leu Glu Asp Arg Thr Gly Lys Val Trp Arg Phe Arg Tyr
 245 250 255

Ser Tyr Trp Asn Ser Ser Gln Ser Tyr Val Leu Thr Lys Gly Trp Ser
 260 265 270

Arg Phe Val Lys Glu Lys Asn Leu Arg Ala Gly Asp Val Val Cys Phe
 275 280 285

Glu Arg Ser Thr Gly Pro Asp Arg Gln Leu Tyr Ile His Trp Lys Val
 290 295 300

Arg Ser Ser Pro Val Gln Thr Val Val Arg Leu Phe Gly Val Asn Ile
 305 310 315 320

Phe Asn Val Ser Asn Glu Lys Pro Asn Asp Val Ala Val Glu Cys Val
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Gly Lys Lys Arg Ser Arg Glu Asp Asp Leu Phe Ser Leu Gly Cys Ser
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Lys Lys Gln Ala Ile Ile Asn Ile Leu
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 20 25 30

Gly Val Arg Lys Arg Pro Trp Gly Arg Tyr Ala Ala Glu Ile Arg Asp
 35 40 45

Pro Val Lys Lys Thr Arg Val Trp Leu Gly Thr Phe Asp Thr Ala Gln
 50 55 60

Gln Ala Ala Arg Ala Tyr Asp Ala Ala Ala Arg Asp Phe Arg Gly Val
 65 70 75 80

Lys Ala Lys Thr Asn Phe Gly Val Ile Val Gly Ser Ser Pro Thr Gln
 85 90 95

Ser Ser Thr Val Val Asp Ser Pro Thr Ala Ala Arg Phe Ile Thr Pro
 100 105 110

Pro His Leu Glu Leu Ser Leu Gly Gly Gly Gly Ala Cys Arg Arg Lys
 115 120 125

Ile Pro Leu Val His Pro Val Tyr Tyr Tyr Asn Met Ala Thr Tyr Pro
 130 135 140

Lys Met Thr Thr Cys Gly Val Gln Ser Glu Ser Glu Thr Ser Ser Val
 145 150 155 160

Val Asp Phe Glu Gly Gly Ala Gly Lys Ile Ser Pro Pro Leu Asp Leu
 165 170 175

Asp Leu Asn Leu Ala Pro Pro Ala Glu
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<223> G1023

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<223> "n" at various positions throughout the sequence
 may be A, T, C, G, other or unknown

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cttgttctggggttaaaggac ttttcttggtcttgagagagttcatttttga ggcttttctg	180
ggaattttgagaggtttttt aggggtttaag gggggttggt tttgaatttc gcacaccaag	240
tgttcgataa a atg gct gaa cga aag aaa cgc tct tct att caa acc aat	290
Met Ala Glu Arg Lys Lys Arg Ser Ser Ile Gln Thr Asn	
1 5 10	
aaa ccc aac aaa aaa ccc atg aag aag aaa cct ttt cag cta aat cac	338
Lys Pro Asn Lys Lys Pro Met Lys Lys Lys Pro Phe Gln Leu Asn His	
15 20 25	
ctc cca ggt tta tct gaa gat ttg aag act atg aga aaa ctc cgt ttc	386
Leu Pro Gly Leu Ser Glu Asp Leu Lys Thr Met Arg Lys Leu Arg Phe	
30 35 40 45	
gtt gtg aat gat cct tac gct act gac tac tca tca agc gaa gaa gaa	434
Val Val Asn Asp Pro Tyr Ala Thr Asp Tyr Ser Ser Ser Glu Glu Glu	
50 55 60	
gaa agg agt cag aga agg aaa cgt tat gtc tgt gag atc gat ctt cct	482
Glu Arg Ser Gln Arg Arg Lys Arg Tyr Val Cys Glu Ile Asp Leu Pro	
65 70 75	
ttc gct caa gct gct act caa gca gaa tct gaa agc tca tat tgt cag	530
Phe Ala Gln Ala Ala Thr Gln Ala Glu Ser Glu Ser Tyr Cys Gln	
80 85 90	
gag agt aac aat aat ggt gta agc aag act aaa atc tca gct tgt agc	578
Glu Ser Asn Asn Asn Gly Val Ser Lys Thr Lys Ile Ser Ala Cys Ser	
95 100 105	
aaa aag gtt tta cgc agc aaa gca tct ccg gtc gtt gga cgt tct tct	626
Lys Lys Val Leu Arg Ser Lys Ala Ser Pro Val Val Gly Arg Ser Ser	
110 115 120 125	
act act gtc tcg aag cct gtt ggt gtt agg cag agg aaa tgg ggt aaa	674
Thr Thr Val Ser Lys Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys	
130 135 140	
tgg gct gct gag att aga cat cca atc acc aaa gta aga act tgg ttg	722
Trp Ala Ala Glu Ile Arg His Pro Ile Thr Lys Val Arg Thr Trp Leu	
145 150 155	
ggt act tac gag acg ctt gaa caa gca gct gat gct tat gct acc aag	770
Gly Thr Tyr Glu Thr Leu Glu Gln Ala Ala Asp Ala Tyr Ala Thr Lys	
160 165 170	
aag ctt gag ttt gat gct ctg gct gca gcc act tct gct gct tcc tct	818
Lys Leu Glu Phe Asp Ala Leu Ala Ala Thr Ser Ala Ala Ser Ser	
175 180 185	
gtt ttg tca aat gag tct ggt tct atg atc tca gcc tca ggg tca agc	866
Val Leu Ser Asn Glu Ser Gly Ser Met Ile Ser Ala Ser Gly Ser Ser	
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 35 40 45
 Asp Pro Tyr Ala Thr Asp Tyr Ser Ser Ser Glu Glu Glu Glu Arg Ser
 50 55 60
 Gln Arg Arg Lys Arg Tyr Val Cys Glu Ile Asp Leu Pro Phe Ala Gln
 65 70 75 80
 Ala Ala Thr Gln Ala Glu Ser Glu Ser Ser Tyr Cys Gln Glu Ser Asn
 85 90 95
 Asn Asn Gly Val Ser Lys Thr Lys Ile Ser Ala Cys Ser Lys Lys Val
 100 105 110
 Leu Arg Ser Lys Ala Ser Pro Val Val Gly Arg Ser Ser Thr Thr Val
 115 120 125
 Ser Lys Pro Val Gly Val Arg Gln Arg Lys Trp Gly Lys Trp Ala Ala
 130 135 140
 Glu Ile Arg His Pro Ile Thr Lys Val Arg Thr Trp Leu Gly Thr Tyr
 145 150 155 160
 Glu Thr Leu Glu Gln Ala Ala Asp Ala Tyr Ala Thr Lys Lys Leu Glu
 165 170 175
 Phe Asp Ala Leu Ala Ala Ala Thr Ser Ala Ala Ser Ser Val Leu Ser
 180 185 190
 Asn Glu Ser Gly Ser Met Ile Ser Ala Ser Gly Ser Ser Ile Asp Leu
 195 200 205
 Asp Lys Lys Leu Val Asp Ser Thr Leu Asp Gln Gln Ala Gly Glu Ser
 210 215 220
 Lys Lys Ala Ser Phe Asp Phe Asp Phe Ala Asp Leu Gln Ile Pro Glu
 225 230 235 240
 Met Gly Cys Phe Ile Asp Asp Ser Phe Ile Pro Asn Ala Cys Glu Leu
 245 250 255
 Asp Phe Leu Leu Thr Glu Glu Asn Asn Asn Gln Met Leu Asp Asp Tyr
 260 265 270
 Cys Gly Ile Asp Asp Leu Asp Ile Ile Gly Leu Glu Cys Asp Gly Pro
 275 280 285
 Ser Glu Leu Pro Asp Tyr Asp Phe Ser Asp Val Glu Ile Asp Leu Gly
 290 295 300

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Leu Ile Gly Thr Thr Ile Asp Lys Tyr Ala Phe Val Asp His Ile Ala
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325 330

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<223> G661

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gacaattata acagtataga gaaggaagaa agaaaagaaa aagaaaccgt tgttgattta 180
gatacagaga agagaagatc atctaac atg gga aga tct cct atc tct gat gac 234
Met Gly Arg Ser Pro Ile Ser Asp Asp
1 5
tct ggt ctc aag aaa ggt cct tgg act cct gat gaa gat gag aaa ctt 282
Ser Gly Leu Lys Lys Gly Pro Trp Thr Pro Asp Glu Asp Glu Lys Leu
10 15 20 25
gtc aac tat gtt caa aaa cat ggt cat agt agc tgg aga gcc ctt ccc 330
Val Asn Tyr Val Gln Lys His Gly His Ser Ser Trp Arg Ala Leu Pro
30 35 40
aaa ctc gct ggt ctt aac agg tgt ggg aag agt tgc agg cta aga tgg 378
Lys Leu Ala Gly Leu Asn Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp
45 50 55
acg aac tac ttg aga cca gac atc aag aga ggg aga ttc tct ccg gac 426
Thr Asn Tyr Leu Arg Pro Asp Ile Lys Arg Gly Arg Phe Ser Pro Asp
60 65 70
gag gaa cag act atc ttg aat ctt cat tca gtt ctt gga aac aag tgg 474
Glu Glu Gln Thr Ile Leu Asn Leu His Ser Val Leu Gly Asn Lys Trp
75 80 85
tca acg att gcg aat cag tta cca ggg aga aca gat aac gag atc aag 522
Ser Thr Ile Ala Asn Gln Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys
90 95 100 105
aat ttc tgg aac act cat ttg aag aag aag ctg att cag atg ggt ttt 570
Asn Phe Trp Asn Thr His Leu Lys Lys Lys Leu Ile Gln Met Gly Phe
110 115 120

gat Asp	cca Pro	atg Met	act Thr	cac His	cgt Arg	cca Pro	aga Arg	acc Thr	gat Asp	atc Ile	ttc Phe	tcc Ser	ggc Gly	tta Leu	tcc Ser		618	
			125						130			135						
cag Gln	ctc Leu	atg Met	tct Ser	ttg Leu	tct Ser	tct Ser	aac Asn	ctg Leu	aga Arg	ggc Gly	ttt Phe	gtt Val	gat Asp	ctg Leu	caa Gln		666	
			140						145			150						
caa Gln	cag Gln	ttt Phe	cct Pro	att Ile	gat Asp	caa Gln	gaa Glu	cac His	act Thr	ata Ile	ctc Leu	aaa Lys	ctc Leu	caa Gln	acc Thr		714	
			155						160			165						
gag Glu	atg Met	gcc Ala	aaa Lys	ctc Leu	caa Gln	ttg Leu	ttc Phe	caa Gln	tac Tyr	ctt Leu	ctt Leu	caa Gln	ccg Pro	tct Ser	tcc Ser		762	
			170						175			180			185			
atg Met	agt Ser	aac Asn	aat Asn	gtt Val	aac Asn	cct Pro	aat Asn	gac Asp	ttt Phe	gac Asp	act Thr	ctc Leu	agt Ser	ctc Leu	ctt Leu		810	
			190						195			200						
aac Asn	tct Ser	att Ile	gcc Ala	tct Ser	ttc Phe	aaa Lys	gag Glu	acc Thr	agt Ser	aat Asn	aat Asn	acc Thr	acc Thr	agc Ser	aac Asn		858	
			205						210			215						
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			220						225			230						
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			235						240			245						
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			250						255			260			265			
gaa Glu	aac Asn	cta Leu	ccc Pro	gtg Val	tct Ser	cca Pro	atc Ile	tgg Trp	ctc Leu	tcg Ser	gat Asp	cca Pro	tcc Ser	agc Ser	aca Thr		1050	
			270						275			280						
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			285						290			295						
gaa Glu	gat Asp	gtc Val	aat Asn	agc Ser	aat Asn	atc Ile	aca Thr	tct Ser	tca Ser	agc Ser	ggc Gly	caa Gln	gaa Glu	tca Ser	gga Gly		1146	
			300						305			310						
gct Ala	tca Ser	gct Ala	tca Ser	gct Ala	gca Ala	tgg Trp	cct Pro	gat Asp	cat His	cta Leu	ttg Leu	gat Asp	gat Asp	tct Ser	ata Ile		1194	
			315						320			325						
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			330															
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Gly	His	Ser 35	Ser	Trp	Arg	Ala	Leu 40	Pro	Lys	Leu	Ala	Gly 45	Leu	Asn	Arg
Cys	Gly 50	Lys	Ser	Cys	Arg	Leu 55	Arg	Trp	Thr	Asn	Tyr 60	Leu	Arg	Pro	Asp
Ile 65	Lys	Arg	Gly	Arg	Phe 70	Ser	Pro	Asp	Glu	Glu 75	Gln	Thr	Ile	Leu	Asn 80
Leu	His	Ser	Val	Leu 85	Gly	Asn	Lys	Trp	Ser 90	Thr	Ile	Ala	Asn	Gln 95	Leu
Pro	Gly	Arg	Thr 100	Asp	Asn	Glu	Ile	Lys 105	Asn	Phe	Trp	Asn	Thr 110	His	Leu
Lys	Lys	Lys 115	Leu	Ile	Gln	Met	Gly 120	Phe	Asp	Pro	Met	Thr 125	His	Arg	Pro
Arg	Thr 130	Asp	Ile	Phe	Ser	Gly 135	Leu	Ser	Gln	Leu	Met 140	Ser	Leu	Ser	Ser
Asn 145	Leu	Arg	Gly	Phe	Val 150	Asp	Leu	Gln	Gln	Gln 155	Phe	Pro	Ile	Asp	Gln 160
Glu	His	Thr	Ile	Leu 165	Lys	Leu	Gln	Thr	Glu 170	Met	Ala	Lys	Leu	Gln 175	Leu
Phe	Gln	Tyr	Leu 180	Leu	Gln	Pro	Ser	Ser 185	Met	Ser	Asn	Asn	Val 190	Asn	Pro
Asn	Asp	Phe 195	Asp	Thr	Leu	Ser	Leu 200	Leu	Asn	Ser	Ile	Ala 205	Ser	Phe	Lys
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<223> G663
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Gly Leu Arg Lys Gly Ala Trp Thr Ala Glu Glu Asp Ser Leu Leu Arg

10 15 20

cta tgt att gat aag tat gga gaa ggc aaa tgg cat caa gtt cct ttg 209
Leu Cys Ile Asp Lys Tyr Gly Glu Gly Lys Trp His Gln Val Pro Leu
25 30 35

aga gct ggg cta aat cga tgc aga aag agt tgt aga cta aga tgg ttg 257
Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser Cys Arg Leu Arg Trp Leu
40 45 50

aac tat ttg aag cca agt atc aag aga gga aga ctt agc aat gat gaa 305
Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly Arg Leu Ser Asn Asp Glu
55 60 65 70

gtt gat ctt ctt ctt cgc ctt cat aag ctt cta gga aat agg tgg tcc 353
Val Asp Leu Leu Leu Arg Leu His Lys Leu Leu Gly Asn Arg Trp Ser
75 80 85

ttg att gct ggt cga ttg cct ggt cgg acc gct aat gat gtc aaa aat 401
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 90 95 100

tac tgg aac acc cat ctg agt aaa aaa cat gag tct tcg tgt tgt aag 449
 Tyr Trp Asn Thr His Leu Ser Lys Lys His Glu Ser Ser Cys Cys Lys
 105 110 115

tct aaa atg aaa aag aaa aac att att tcc cct cct aca aca ccg gtc 497
 Ser Lys Met Lys Lys Lys Asn Ile Ile Ser Pro Pro Thr Thr Pro Val
 120 125 130

caa aaa atc ggt gtt ttt aag cct cga cct cga tcc ttc tct gtt aac 545
 Gln Lys Ile Gly Val Phe Lys Pro Arg Pro Arg Ser Phe Ser Val Asn
 135 140 145 150

aat ggt tgc agc cat ctc aat ggt ctg cca gaa gtt gat tta att cct 593
 Asn Gly Cys Ser His Leu Asn Gly Leu Pro Glu Val Asp Leu Ile Pro
 155 160 165

tca tgc ctt gga ctc aag aaa aat aat gtt tgt gaa aat agt atc aca 641
 Ser Cys Leu Gly Leu Lys Lys Asn Asn Val Cys Glu Asn Ser Ile Thr
 170 175 180

tgt aac aaa gat gat gag aaa gat gat ttt gtg aat aat cta atg aat 689
 Cys Asn Lys Asp Asp Glu Lys Asp Asp Phe Val Asn Asn Leu Met Asn
 185 190 195

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 Gly Asp Asn Met Trp Leu Glu Asn Leu Leu Gly Glu Asn Gln Glu Ala
 200 205 210

gat gcg att gtt cct gaa gcg acg aca gct gaa cat ggg gcc act ttg 785
 Asp Ala Ile Val Pro Glu Ala Thr Thr Ala Glu His Gly Ala Thr Leu
 215 220 225 230

gcg ttt gac gtt gag caa ctt tgg agt ctg ttt gat gga gag act gtt 833
 Ala Phe Asp Val Glu Gln Leu Trp Ser Leu Phe Asp Gly Glu Thr Val
 235 240 245

gaa ctt gat tagtggttct caccgtttgt ttaagattgt ggggtggcttt 882
 Glu Leu Asp

tctttcgtat tttagtaatg tatttttctg tatgaagtaa agaatttcag cattttaaga 942

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Trp His Gln Val Pro Leu Arg Ala Gly Leu Asn Arg Cys Arg Lys Ser
 35 40 45

Cys Arg Leu Arg Trp Leu Asn Tyr Leu Lys Pro Ser Ile Lys Arg Gly
 50 55 60

Arg Leu Ser Asn Asp Glu Val Asp Leu Leu Leu Arg Leu His Lys Leu
 65 70 75 80

Leu Gly Asn Arg Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
 85 90 95

Ala Asn Asp Val Lys Asn Tyr Trp Asn Thr His Leu Ser Lys Lys His
 100 105 110

Glu Ser Ser Cys Cys Lys Ser Lys Met Lys Lys Lys Asn Ile Ile Ser
 115 120 125

Pro Pro Thr Thr Pro Val Gln Lys Ile Gly Val Phe Lys Pro Arg Pro
 130 135 140

Arg Ser Phe Ser Val Asn Asn Gly Cys Ser His Leu Asn Gly Leu Pro
 145 150 155 160

Glu Val Asp Leu Ile Pro Ser Cys Leu Gly Leu Lys Lys Asn Asn Val
 165 170 175

Cys Glu Asn Ser Ile Thr Cys Asn Lys Asp Asp Glu Lys Asp Asp Phe
 180 185 190

Val Asn Asn Leu Met Asn Gly Asp Asn Met Trp Leu Glu Asn Leu Leu
 195 200 205

Gly Glu Asn Gln Glu Ala Asp Ala Ile Val Pro Glu Ala Thr Thr Ala
 210 215 220

Glu His Gly Ala Thr Leu Ala Phe Asp Val Glu Gln Leu Trp Ser Leu
 225 230 235 240

Phe Asp Gly Glu Thr Val Glu Leu Asp
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ccg tgc tgt gag aaa gct cac aca aac aaa gga gca tgg acg aaa gaa 163
Pro Cys Cys Glu Lys Ala His Thr Asn Lys Gly Ala Trp Thr Lys Glu
5 10 15 20

gag gac gag agg ctc gtc gcc tac att aaa gct cat gga gaa ggc tgc 211
Glu Asp Glu Arg Leu Val Ala Tyr Ile Lys Ala His Gly Glu Gly Cys
25 30 35

tgg aga tct ctc ccc aaa gcc gcc gga ctt ctt cgc tgt ggc aag agc 259
Trp Arg Ser Leu Pro Lys Ala Ala Gly Leu Leu Arg Cys Gly Lys Ser

40 45 50

tgc cgt ctc cgg tgg atc aac tat ctc cgg cct gac ctt aag cgt gga 307
Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly
55 60 65

aac ttc acc gag gaa gaa gac gaa ctc atc atc aag ctc cat agc ctt 355
Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys Leu His Ser Leu
70 75 80

ctt ggc aac aaa tgg tcg ctt att gcc ggg aga tta ccg gga aga aca 403
Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu Pro Gly Arg Thr
85 90 95 100

gat aac gag ata aag aac tat tgg aac acg cat ata cga aga aag ctt 451
Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile Arg Arg Lys Leu
105 110 115

ata aac aga ggg att gat cca acg agt cat aga cca atc caa gaa tca 499
Ile Asn Arg Gly Ile Asp Pro Thr Ser His Arg Pro Ile Gln Glu Ser
120 125 130

tca gct tct caa gat tct aaa cct aca caa cta gaa cca gtt acg agt 547
Ser Ala Ser Gln Asp Ser Lys Pro Thr Gln Leu Glu Pro Val Thr Ser
135 140 145

aat acc att aat atc tca ttc act tct gct cca aag gtc gaa acg ttc 595
Asn Thr Ile Asn Ile Ser Phe Thr Ser Ala Pro Lys Val Glu Thr Phe
150 155 160

cat gaa agt ata agc ttt ccg gga aaa tca gag aaa atc tca atg ctt 643
His Glu Ser Ile Ser Phe Pro Gly Lys Ser Glu Lys Ile Ser Met Leu
165 170 175 180

acg ttc aaa gaa gaa aaa gat gag tgc cca gtt caa gaa aag ttc cca 691
Thr Phe Lys Glu Glu Lys Asp Glu Cys Pro Val Gln Glu Lys Phe Pro
185 190 195

gat ttg aat ctt gag ctc aga atc agt ctt cct gat gat gtt gat cgt 739
Asp Leu Asn Leu Glu Leu Arg Ile Ser Leu Pro Asp Asp Val Asp Arg
200 205 210

ctt caa ggg cat gga aag tca aca acg cca cgt tgt ttc aag tgc agc 787
Leu Gln Gly His Gly Lys Ser Thr Thr Pro Arg Cys Phe Lys Cys Ser
215 220 225

tta ggg atg ata aac ggc atg gag tgc aga tgc gga aga atg aga tgc 835
Leu Gly Met Ile Asn Gly Met Glu Cys Arg Cys Gly Arg Met Arg Cys
230 235 240

gat gta gtc gga ggt agc agc aag ggg agt gac atg agc aat gga ttt 883
Asp Val Val Gly Gly Ser Ser Lys Gly Ser Asp Met Ser Asn Gly Phe
245 250 255 260

gat ttt tta ggg ttg gca aag aaa gag acc act tct ctt ttg ggc ttt 931
Asp Phe Leu Gly Leu Ala Lys Lys Glu Thr Thr Ser Leu Leu Gly Phe
265 270 275

cga agc ttg gag atg aaataatatt gtcaaatttt aggcgtaact gtacaaaact 986
Arg Ser Leu Glu Met
280

tttgcctaga taatttgaaa gtatatcttc aacttgtatg agaaatttaa ctgggtgaatt 1046

ataatatata gaatttgttt tttaaaaaaaa aaaaaaaaaa a 1087

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35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
50 55 60

Leu Lys Arg Gly Asn Phe Thr Glu Glu Glu Asp Glu Leu Ile Ile Lys
65 70 75 80

Leu His Ser Leu Leu Gly Asn Lys Trp Ser Leu Ile Ala Gly Arg Leu
85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His Ile
100 105 110

Arg Arg Lys Leu Ile Asn Arg Gly Ile Asp Pro Thr Ser His Arg Pro
115 120 125

Ile Gln Glu Ser Ser Ala Ser Gln Asp Ser Lys Pro Thr Gln Leu Glu
130 135 140

Pro Val Thr Ser Asn Thr Ile Asn Ile Ser Phe Thr Ser Ala Pro Lys
145 150 155 160

Val Glu Thr Phe His Glu Ser Ile Ser Phe Pro Gly Lys Ser Glu Lys
165 170 175

Ile Ser Met Leu Thr Phe Lys Glu Glu Lys Asp Glu Cys Pro Val Gln
180 185 190

Glu Lys Phe Pro Asp Leu Asn Leu Glu Leu Arg Ile Ser Leu Pro Asp
195 200 205

Asp Val Asp Arg Leu Gln Gly His Gly Lys Ser Thr Thr Pro Arg Cys
210 215 220

Phe Lys Cys Ser Leu Gly Met Ile Asn Gly Met Glu Cys Arg Cys Gly
225 230 235 240

Arg Met Arg Cys Asp Val Val Gly Gly Ser Ser Lys Gly Ser Asp Met
245 250 255

Ser Asn Gly Phe Asp Phe Leu Gly Leu Ala Lys Lys Glu Thr Thr Ser
260 265 270

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ggt atg act cgt cga tgt tct cac tgc aat cac aat ggc cac aac tct 168
Met Thr Arg Arg Cys Ser His Cys Asn His Asn Gly His Asn Ser
1 5 10 15

cgg act tgt ccc aat cgc ggc gtg aag ctc ttt ggt gtt cgg ctc acc 216
Arg Thr Cys Pro Asn Arg Gly Val Lys Leu Phe Gly Val Arg Leu Thr
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gaa ggt tcg atc cgg aaa agt gca agt atg ggt aat ctt agc cat tac	264
Glu Gly Ser Ile Arg Lys Ser Ala Ser Met Gly Asn Leu Ser His Tyr	
35 40 45	
acg ggt tct gga tcg ggt ggg cat gga acc ggg tcc aac act ccg ggt	312
Thr Gly Ser Gly Ser Gly Gly His Gly Thr Gly Ser Asn Thr Pro Gly	
50 55 60	
tct ccg ggt gat gtc cct gac cat gtc gct ggt gat ggt tac gct tct	360
Ser Pro Gly Asp Val Pro Asp His Val Ala Gly Asp Gly Tyr Ala Ser	
65 70 75	
gag gat ttc gtt gct ggc tct tcc tct agc cgc gag aga aag aaa gga	408
Glu Asp Phe Val Ala Gly Ser Ser Ser Ser Arg Glu Arg Lys Lys Gly	
80 85 90 95	
act cca tgg aca gag gaa gaa cac agg atg ttc tta tta ggt tta cag	456
Thr Pro Trp Thr Glu Glu Glu His Arg Met Phe Leu Leu Gly Leu Gln	
100 105 110	
aag ctg ggt aaa ggt gat tgg aga ggt atc tca aga aac tat gtg acc	504
Lys Leu Gly Lys Gly Asp Trp Arg Gly Ile Ser Arg Asn Tyr Val Thr	
115 120 125	
act agg aca cct aca caa gtt gct agc cat gct cag aag tat ttc atc	552
Thr Arg Thr Pro Thr Gln Val Ala Ser His Ala Gln Lys Tyr Phe Ile	
130 135 140	
aga caa tcc aat gtc tct cgt cgc aaa aga cgt tct agt ctc ttt gat	600
Arg Gln Ser Asn Val Ser Arg Arg Lys Arg Arg Ser Ser Leu Phe Asp	
145 150 155	
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Met Val Pro Asp Glu Val Gly Asp Ile Pro Met Asp Leu Gln Glu Pro	
160 165 170 175	
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Glu Glu Asp Asn Ile Pro Val Glu Thr Glu Met Gln Gly Ala Asp Ser	
180 185 190	
att cat cag aca ctt gct cct agc tca ctt cac gca ccg tca atc ttg	744
Ile His Gln Thr Leu Ala Pro Ser Ser Leu His Ala Pro Ser Ile Leu	
195 200 205	
gaa atc gaa gaa tgt gaa tca atg gac tcc aca aac tct acc acc ggg	792
Glu Ile Glu Glu Cys Glu Ser Met Asp Ser Thr Asn Ser Thr Thr Gly	
210 215 220	
gaa cca acc gca act gcc gct gct gct tct tct tct tcc aga cta gaa	840
Glu Pro Thr Ala Thr Ala Ala Ala Ser Ser Ser Ser Arg Leu Glu	
225 230 235	
gaa acc aca caa ctg caa tca caa ctg caa ccg cag ccg caa cta cct	888
Glu Thr Thr Gln Leu Gln Ser Gln Leu Gln Pro Gln Pro Gln Leu Pro	
240 245 250 255	

ggc tca ttc ccc ata cta tat ccg acc tac ttt tca cca tat tac ccg	936
Gly Ser Phe Pro Ile Leu Tyr Pro Thr Tyr Phe Ser Pro Tyr Tyr Pro	
260 265 270	
ttt cca ttc cca ata tgg cct gct ggt tat gtt cct gaa cca ccc aag	984
Phe Pro Phe Pro Ile Trp Pro Ala Gly Tyr Val Pro Glu Pro Pro Lys	
275 280 285	
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Lys Glu Glu Thr His Glu Ile Leu Arg Pro Thr Ala Val His Ser Lys	
290 295 300	
gct cct atc aat gtt gac gag ctt ctt ggt atg tct aag ctc agc ctt	1080
Ala Pro Ile Asn Val Asp Glu Leu Leu Gly Met Ser Lys Leu Ser Leu	
305 310 315	
gca gag tcc aac aaa cat gga gaa tcc gat cag tct ctt tca ttg aag	1128
Ala Glu Ser Asn Lys His Gly Glu Ser Asp Gln Ser Leu Ser Leu Lys	
320 325 330 335	
cta ggt ggc ggg tca tct tca aga caa tca gca ttt cac ccg aat cct	1176
Leu Gly Gly Gly Ser Ser Ser Arg Gln Ser Ala Phe His Pro Asn Pro	
340 345 350	
agc tct gat agt tca gac atc aaa agc gtg ata cac gct tta	1218
Ser Ser Asp Ser Ser Asp Ile Lys Ser Val Ile His Ala Leu	
355 360 365	
taaaagacct gaggaagtga tggtctaaaa tgggatctgg tttggggttt acagggttagt	1278
tgttgggtcac agtaacttaa ataagttttt ctttggttagg ttgtttaact tgggtaggat	1338
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Gly Ser Ile Arg Lys Ser Ala Ser Met Gly Asn Leu Ser His Tyr Thr	
35 40 45	
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gat tct aag ggt ttg aga ctg gcg aaa caa gct ccc tca atg cat ggt 735
 Asp Ser Lys Gly Leu Arg Leu Ala Lys Gln Ala Pro Ser Met His Gly
 210 215 220

ctt cct gat ttt gct gag gtt tat aac ttc att ggg agt gtg ttc gat 783
 Leu Pro Asp Phe Ala Glu Val Tyr Asn Phe Ile Gly Ser Val Phe Asp
 225 230 235

cct gac agc aaa ggc cgc atg aaa aag ctc aag gaa atg gat cct ata 831
 Pro Asp Ser Lys Gly Arg Met Lys Lys Leu Lys Glu Met Asp Pro Ile
 240 245 250

aat ttc gaa act gtt ttg ctg ttg atg aga aac ctc aca gtg aac ttg 879
 Asn Phe Glu Thr Val Leu Leu Leu Met Arg Asn Leu Thr Val Asn Leu
 255 260 265

tca aac cct gac ttt gaa cct act tct gaa tat gtt gat gct gca gag 927
 Ser Asn Pro Asp Phe Glu Pro Thr Ser Glu Tyr Val Asp Ala Ala Glu
 270 275 280 285

gaa ggt cat gaa cac tta agc tct tagctgtttg tgcactcaac aagttatata 981
 Glu Gly His Glu His Leu Ser Ser
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tcttcttgac gacttcttgc tcgcaacaac tctctaccag ctatcaaagc catcgtagcg 1041

ttgttgtctg aggagaacat aactgagtcg tcgtcacaaa caagaggaac atatgcagtt 1101

tcggtcagaa ccagtcgtgt gaatggtaga tatatgtatg tgtgtgtaga aaatgggttac 1161

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 35 40 45

Glu Ser Trp Thr Glu Gly Glu His Asp Lys Phe Leu Glu Ala Leu Gln
 50 55 60
 Leu Phe Asp Arg Asp Trp Lys Lys Ile Glu Asp Phe Val Gly Ser Lys
 65 70 75 80
 Thr Val Ile Gln Ile Arg Ser His Ala Gln Lys Tyr Phe Leu Lys Val
 85 90 95
 Gln Lys Asn Gly Thr Leu Ala His Val Pro Pro Pro Arg Pro Lys Arg
 100 105 110
 Lys Ala Ala His Pro Tyr Pro Gln Lys Ala Ser Lys Asn Ala Gln Met
 115 120 125
 Ser Leu His Val Ser Met Ser Phe Pro Thr Gln Ile Asn Asn Leu Pro
 130 135 140
 Gly Tyr Thr Pro Trp Asp Asp Asp Thr Ser Ala Leu Leu Asn Ile Ala
 145 150 155 160
 Val Ser Gly Val Ile Pro Pro Glu Asp Glu Leu Asp Thr Leu Cys Gly
 165 170 175
 Ala Glu Val Asp Val Gly Ser Asn Asp Met Ile Ser Glu Thr Ser Pro
 180 185 190
 Ser Ala Ser Gly Ile Gly Ser Ser Ser Arg Thr Leu Ser Asp Ser Lys
 195 200 205
 Gly Leu Arg Leu Ala Lys Gln Ala Pro Ser Met His Gly Leu Pro Asp
 210 215 220
 Phe Ala Glu Val Tyr Asn Phe Ile Gly Ser Val Phe Asp Pro Asp Ser
 225 230 235 240
 Lys Gly Arg Met Lys Lys Leu Lys Glu Met Asp Pro Ile Asn Phe Glu
 245 250 255
 Thr Val Leu Leu Leu Met Arg Asn Leu Thr Val Asn Leu Ser Asn Pro
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 Glu His Leu Ser Ser
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Pro Trp Thr Pro Glu Glu Asp Gln Lys Leu Ile Asp Tyr Ile His Lys	
20 25 30	
cat ggt cat gga agc tgg aga gct ctc ccc aag ctc gca gat ttg aat	143
His Gly His Gly Ser Trp Arg Ala Leu Pro Lys Leu Ala Asp Leu Asn	
35 40 45	
agg tgt gga aag agt tgt aga ctg agg tgg aca aat tat ttg aga cca	191
Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro	
50 55 60	
gac atc aaa aga gga aag ttt tca gcc gaa gaa gag caa aca atc ctc	239
Asp Ile Lys Arg Gly Lys Phe Ser Ala Glu Glu Glu Gln Thr Ile Leu	
65 70 75	
cat ctc cac tcc att ctc ggg aat aaa tgg tca gct att gcg acg cat	287
His Leu His Ser Ile Leu Gly Asn Lys Trp Ser Ala Ile Ala Thr His	
80 85 90 95	
ttg caa ggt cgt aca gat aat gag ata aaa aac ttt tgg aac aca cat	335
Leu Gln Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Asn Thr His	
100 105 110	
cta aag aag aaa ttg atc cag atg ggg atc gat cct gtg act cat cag	383
Leu Lys Lys Lys Leu Ile Gln Met Gly Ile Asp Pro Val Thr His Gln	
115 120 125	
cca aga acc gac ctc ttc gca agt tta cct cag ctc ata gcc ttg gca	431
Pro Arg Thr Asp Leu Phe Ala Ser Leu Pro Gln Leu Ile Ala Leu Ala	
130 135 140	
aat cta aaa gac cta atc gaa caa aca tca caa ttc tca tcc atg caa	479
Asn Leu Lys Asp Leu Ile Glu Gln Thr Ser Gln Phe Ser Ser Met Gln	
145 150 155	
ggc gaa gca gcc caa cta gcc aat cta caa tat ctc caa cgt atg ttt	527
Gly Glu Ala Ala Gln Leu Ala Asn Leu Gln Tyr Leu Gln Arg Met Phe	
160 165 170 175	
aat tct tcg gct tca tta acc aac aac aac ggc aac aat ttt agc ccg	575
Asn Ser Ser Ala Ser Leu Thr Asn Asn Asn Gly Asn Asn Phe Ser Pro	
180 185 190	
agt agt att ctc gat atc gat cag cac cat gcc atg aac ctc tta aac	623
Ser Ser Ile Leu Asp Ile Asp Gln His His Ala Met Asn Leu Leu Asn	
195 200 205	
tcc atg gtc tct tgg aac aaa gat caa aac ccc gct ttt gat ccg gtt	671
Ser Met Val Ser Trp Asn Lys Asp Gln Asn Pro Ala Phe Asp Pro Val	
210 215 220	

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 225 230 235
 ttt atc att gat caa ccc acc caa cca ctc caa caa caa aaa tac cat 767
 Phe Ile Ile Asp Gln Pro Thr Gln Pro Leu Gln Gln Gln Lys Tyr His
 240 245 250 255
 tta aac aat agt cct agt gag cta cca tcg caa ggt gac cca ctt ctt 815
 Leu Asn Asn Ser Pro Ser Glu Leu Pro Ser Gln Gly Asp Pro Leu Leu
 260 265 270
 gat cat gtc cct ttc agt ctc caa aca cct ttg aat agt gag gat cac 863
 Asp His Val Pro Phe Ser Leu Gln Thr Pro Leu Asn Ser Glu Asp His
 275 280 285
 ttt ata gat aat ttg gtc aaa cat cca act gat cat gag cat gaa cat 911
 Phe Ile Asp Asn Leu Val Lys His Pro Thr Asp His Glu His Glu His
 290 295 300
 gat gac aat cca tct tca tgg gtt ctc cct tct ctt ata gac aat aac 959
 Asp Asp Asn Pro Ser Ser Trp Val Leu Pro Ser Leu Ile Asp Asn Asn
 305 310 315
 cct aaa act gtc acg tct tct ctt cca cac aac aat ccg gcg gat gca 1007
 Pro Lys Thr Val Thr Ser Ser Leu Pro His Asn Asn Pro Ala Asp Ala
 320 325 330 335
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 Ser Ser Ser Ser Ser Tyr Gly Gly Cys Glu Ala Ala Ser Phe Tyr Trp
 340 345 350
 cct gac att tgc ttc gac gaa agc ctc atg aac gtt ata tct 1097
 Pro Asp Ile Cys Phe Asp Glu Ser Leu Met Asn Val Ile Ser
 355 360 365
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 35 40 45
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
 50 55 60
 Ile Lys Arg Gly Lys Phe Ser Ala Glu Glu Glu Gln Thr Ile Leu His
 65 70 75 80
 Leu His Ser Ile Leu Gly Asn Lys Trp Ser Ala Ile Ala Thr His Leu
 85 90 95
 Gln Gly Arg Thr Asp Asn Glu Ile Lys Asn Phe Trp Asn Thr His Leu
 100 105 110
 Lys Lys Lys Leu Ile Gln Met Gly Ile Asp Pro Val Thr His Gln Pro
 115 120 125
 Arg Thr Asp Leu Phe Ala Ser Leu Pro Gln Leu Ile Ala Leu Ala Asn
 130 135 140
 Leu Lys Asp Leu Ile Glu Gln Thr Ser Gln Phe Ser Ser Met Gln Gly
 145 150 155 160
 Glu Ala Ala Gln Leu Ala Asn Leu Gln Tyr Leu Gln Arg Met Phe Asn
 165 170 175
 Ser Ser Ala Ser Leu Thr Asn Asn Asn Gly Asn Asn Phe Ser Pro Ser
 180 185 190
 Ser Ile Leu Asp Ile Asp Gln His His Ala Met Asn Leu Leu Asn Ser
 195 200 205
 Met Val Ser Trp Asn Lys Asp Gln Asn Pro Ala Phe Asp Pro Val Leu
 210 215 220
 Glu Leu Glu Ala Asn Asp Gln Asn Gln Asp Leu Phe Pro Leu Gly Phe
 225 230 235 240
 Ile Ile Asp Gln Pro Thr Gln Pro Leu Gln Gln Gln Lys Tyr His Leu
 245 250 255
 Asn Asn Ser Pro Ser Glu Leu Pro Ser Gln Gly Asp Pro Leu Leu Asp
 260 265 270
 His Val Pro Phe Ser Leu Gln Thr Pro Leu Asn Ser Glu Asp His Phe
 275 280 285
 Ile Asp Asn Leu Val Lys His Pro Thr Asp His Glu His Glu His Asp
 290 295 300
 Asp Asn Pro Ser Ser Trp Val Leu Pro Ser Leu Ile Asp Asn Asn Pro
 305 310 315 320

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aattgtcata	gaaccaattc	agagagaacg	agagagagag	agagagaa	atg ggg aga	177										
					Met Gly Arg											
					1											
caa cca tgc tgt gac aaa gta ggg ttg aag aaa gga cca tgg act gca											225					
Gln Pro Cys Cys Asp Lys Val Gly Leu Lys Lys Gly Pro Trp Thr Ala																
5	10										15					
gaa gag gat agg aag ctc ata aac ttc atc ctt acc aat gga caa tgt											273					
Glu Glu Asp Arg Lys Leu Ile Asn Phe Ile Leu Thr Asn Gly Gln Cys																
20	25										30	35				
tgt tgg aga gct gtt cct aag ctt tct ggt ctt ctt agg tgt ggc aag											321					
Cys Trp Arg Ala Val Pro Lys Leu Ser Gly Leu Leu Arg Cys Gly Lys																
40					45					50						
agt tgc aga ctt cgt tgg act aac tat ctt aga cca gac ctt aag aga											369					
Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp Leu Lys Arg																
55					60					65						
ggt ctt ctc tct gat tac gaa gag aag atg gtc att gat ctc cat tcc											417					
Gly Leu Leu Ser Asp Tyr Glu Glu Lys Met Val Ile Asp Leu His Ser																
70				75					80							
cag ctt gga aac agg tgg tca aag ata gct tct cat tta cca gga aga											465					
Gln Leu Gly Asn Arg Trp Ser Lys Ile Ala Ser His Leu Pro Gly Arg																
85				90					95							
aca gac aac gaa atc aag aat cat tgg aac act cac atc aag aag aag											513					
Thr Asp Asn Glu Ile Lys Asn His Trp Asn Thr His Ile Lys Lys Lys																
100				105					110					115		

ttg agg aaa atg ggg att gat cct ctt aca cat aaa cca ctc tct atc 561
 Leu Arg Lys Met Gly Ile Asp Pro Leu Thr His Lys Pro Leu Ser Ile
 120 125 130

gtc gaa aaa gaa gac gaa gaa ccc tta aag aag cta cag aat aat aca 609
 Val Glu Lys Glu Asp Glu Glu Pro Leu Lys Lys Leu Gln Asn Asn Thr
 135 140 145

gtt cct ttt caa gaa aca atg gag cgt cct tta gag aac aac atc aag 657
 Val Pro Phe Gln Glu Thr Met Glu Arg Pro Leu Glu Asn Asn Ile Lys
 150 155 160

aac ata tca aga ctt gaa gag tct tta ggt gat gat caa ttc atg gag 705
 Asn Ile Ser Arg Leu Glu Glu Ser Leu Gly Asp Asp Gln Phe Met Glu
 165 170 175

ata aat ctt gag tat ggt gtc gaa gat gtc cct ctt att gaa aca gag 753
 Ile Asn Leu Glu Tyr Gly Val Glu Asp Val Pro Leu Ile Glu Thr Glu
 180 185 190 195

tct tta gac ctt atc tgc agc aat tca aca atg tct tca tcc acg tcc 801
 Ser Leu Asp Leu Ile Cys Ser Asn Ser Thr Met Ser Ser Ser Thr Ser
 200 205 210

aca tct tcg cat tct tct aat gat tcg agt ttc ttg aag gat ttg cag 849
 Thr Ser Ser His Ser Ser Asn Asp Ser Ser Phe Leu Lys Asp Leu Gln
 215 220 225

ttc ccg gag ttc gag tgg tcc gac tat ggt aat agt aat aat gat aat 897
 Phe Pro Glu Phe Glu Trp Ser Asp Tyr Gly Asn Ser Asn Asn Asp Asn
 230 235 240

aat aat ggt gtg gac aac att ata gag aac aat atg atg agc ctg tgg 945
 Asn Asn Gly Val Asp Asn Ile Ile Glu Asn Asn Met Met Ser Leu Trp
 245 250 255

gaa att agt gac ttt agc agt ttg gat ttg ctg ctt aat gat gag agt 993
 Glu Ile Ser Asp Phe Ser Ser Leu Asp Leu Leu Leu Asn Asp Glu Ser
 260 265 270 275

tct tcc act ttt ggg ttg ttt tgaattcatt cttaagaata tggtttcttt 1044
 Ser Ser Thr Phe Gly Leu Phe
 280

tgtaaaagaa tggaaactat tgggggtgggg gaaacagaaa aacctaaata cccttcgtta 1104

ctctagtttt tgagggatatt gagagaacgt ttttttactt gtgagaaatt tagaaacaaa 1164

aataaagttt atttattttg tac 1187

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<213> Arabidopsis thaliana

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Gly Gln Cys Cys Trp Arg Ala Val Pro Lys Leu Ser Gly Leu Leu Arg
 35 40 45

Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Asp
 50 55 60

Leu Lys Arg Gly Leu Leu Ser Asp Tyr Glu Glu Lys Met Val Ile Asp
 65 70 75 80

Leu His Ser Gln Leu Gly Asn Arg Trp Ser Lys Ile Ala Ser His Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn His Trp Asn Thr His Ile
 100 105 110

Lys Lys Lys Leu Arg Lys Met Gly Ile Asp Pro Leu Thr His Lys Pro
 115 120 125

Leu Ser Ile Val Glu Lys Glu Asp Glu Glu Pro Leu Lys Lys Leu Gln
 130 135 140

Asn Asn Thr Val Pro Phe Gln Glu Thr Met Glu Arg Pro Leu Glu Asn
 145 150 155 160

Asn Ile Lys Asn Ile Ser Arg Leu Glu Glu Ser Leu Gly Asp Asp Gln
 165 170 175

Phe Met Glu Ile Asn Leu Glu Tyr Gly Val Glu Asp Val Pro Leu Ile
 180 185 190

Glu Thr Glu Ser Leu Asp Leu Ile Cys Ser Asn Ser Thr Met Ser Ser
 195 200 205

Ser Thr Ser Thr Ser Ser His Ser Ser Asn Asp Ser Ser Phe Leu Lys
 210 215 220

Asp Leu Gln Phe Pro Glu Phe Glu Trp Ser Asp Tyr Gly Asn Ser Asn
 225 230 235 240

Asn Asp Asn Asn Asn Gly Val Asp Asn Ile Ile Glu Asn Asn Met Met
 245 250 255

Ser Leu Trp Glu Ile Ser Asp Phe Ser Ser Leu Asp Leu Leu Leu Asn
 260 265 270

Asp Glu Ser Ser Ser Thr Phe Gly Leu Phe
 275 280

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Asp Cys Gly Val Thr Gly Lys Arg Asp Glu Ile Met Leu Phe Gly Val
15 20 25

tct gat tat gaa aag tct tct ccg gag gat gag atc cct aag ata gtc 257
Ser Asp Tyr Glu Lys Ser Ser Pro Glu Asp Glu Ile Pro Lys Ile Val
45 50 55

gtg att gtc gct gac ggt tac gcc tcc gcc aat gac gct gtc cag att 353
Val Ile Val Ala Asp Gly Tyr Ala Ser Ala Asn Asp Ala Val Gln Ile
80 85 90

gag cat aag agg ttc ttg att ggg ttg cag aaa gta gga aaa gga gat 449
Glu His Lys Arg Phe Leu Ile Gly Leu Gln Lys Val Gly Lys Gly Asp
110 115 120

gta gct agt cat gct cag aaa tac ttc ctc cga cga acc aac ctc aac	545
Val Ala Ser His Ala Gln Lys Tyr Phe Leu Arg Arg Thr Asn Leu Asn	
140	145 150 155

cgt cgc cga aga aga tct agc ctt ttt gat atc act act gag acg gtt 593
 Arg Arg Arg Arg Arg Ser Ser Leu Phe Asp Ile Thr Thr Glu Thr Val
 160 165 170

aca gaa atg gcc atg gag caa gat cct act cag gag aac tca cca cta 641
 Thr Glu Met Ala Met Glu Gln Asp Pro Thr Gln Glu Asn Ser Pro Leu
 175 180 185

cct gaa acc aac atc agc tct gga cag caa gcg atg caa gtt ttt act 689
 Pro Glu Thr Asn Ile Ser Ser Gly Gln Gln Ala Met Gln Val Phe Thr
 190 195 200

gac gtg gcc gac aaa aac tgagaatgca ccagagacat ttcattctcaa 737
 Asp Val Ala Asp Lys Asn
 205

cgatccatat ctggttccag taaccttcca agcaaagcca acattcaatc taaacacaga 797

tgctgtccca ctttctctca acctttgtct ggcattctca tttaatctta acgagcaacc 857

caactcaaga cactcggctt tcacgatgat gccaaagcttc agcgatggag atagcaatag 917

cagcatcatc agagttgctt agagcttaaa cccaagggga atctacaaga acctgggttct 977

ttctttgggt ctctggtggt gggaggacta agnagtacct attagngtt aacagattng 1037

aaaaaa 1043

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<213> Arabidopsis thaliana

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Pro Met Arg Lys Cys Val Ser Leu Asn Asn Leu Ser Asp Tyr Glu Lys
 35 40 45

Ser Ser Pro Glu Asp Glu Ile Pro Lys Ile Val Thr Ala Gly Ala Gly
 50 55 60

Asp Gly Glu Asp Lys Asn Glu Thr Asp Ala Thr Val Ile Val Ala Asp
 65 70 75 80

Gly Tyr Ala Ser Ala Asn Asp Ala Val Gln Ile Ser Ser Ser Ser Gly
 85 90 95

Gly Arg Lys Arg Gly Val Pro Trp Thr Glu Asn Glu His Lys Arg Phe
 100 105 110

Leu Ile Gly Leu Gln Lys Val Gly Lys Gly Asp Trp Lys Gly Ile Ser
115 120 125

Arg Asn Phe Val Lys Ser Arg Thr Pro Thr Gln Val Ala Ser His Ala
130 135 140

Gln Lys Tyr Phe Leu Arg Arg Thr Asn Leu Asn Arg Arg Arg Arg Arg
145 150 155 160

Ser Ser Leu Phe Asp Ile Thr Thr Glu Thr Val Thr Glu Met Ala Met
165 170 175

Glu Gln Asp Pro Thr Gln Glu Asn Ser Pro Leu Pro Glu Thr Asn Ile
180 185 190

Ser Ser Gly Gln Gln Ala Met Gln Val Phe Thr Asp Val Ala Asp Lys
195 200 205

Asn

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<223> G932

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tctctctgct cataccacaa accgttccat tcttccccta atcacaaagt gatatttaca 180
tagagaagat agag atg gga aga cca cca tgc tgt gac aag att gga gtg 230
Met Gly Arg Pro Pro Cys Cys Asp Lys Ile Gly Val
1 5 10
aag aaa gga cca tgg aca cca gag gaa gat atc atc ttg gtt tct tac 278
Lys Lys Gly Pro Trp Thr Pro Glu Glu Asp Ile Ile Leu Val Ser Tyr
15 20 25
atc caa gaa cat ggt cct gga aac tgg aga tct gtg cct act cac aca 326
Ile Gln Glu His Gly Pro Gly Asn Trp Arg Ser Val Pro Thr His Thr
30 35 40
ggg ttg agg aga tgt agc aaa agc tgt aga ttg agg tgg act aat tat 374
Gly Leu Arg Arg Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr
45 50 55 60

666150:51466660

ctt cga cct ggg atc aag cgt gga aat ttc acc gag cat gaa gag aag 422
 Leu Arg Pro Gly Ile Lys Arg Gly Asn Phe Thr Glu His Glu Glu Lys
 65 70 75

atg att ctc cat ctt caa gct ctt ttg gga aac agg tgg gca gct ata 470
 Met Ile Leu His Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile
 80 85 90

gca tca tat ctt cca gaa agg aca gac aat gat ata aag aac tat tgg 518
 Ala Ser Tyr Leu Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp
 95 100 105

aac act cat ttg aag aaa aag ctc aag aag atg aat gat tct tgt gat 566
 Asn Thr His Leu Lys Lys Lys Leu Lys Lys Met Asn Asp Ser Cys Asp
 110 115 120

agt act atc aac aat ggc ctt gat aat aaa gac ttc tcc ata tca aac 614
 Ser Thr Ile Asn Asn Gly Leu Asp Asn Lys Asp Phe Ser Ile Ser Asn
 125 130 135 140

aaa aac act acc tca cat caa agc agc aac tcc agt aaa ggt caa tgg 662
 Lys Asn Thr Thr Ser His Gln Ser Ser Asn Ser Ser Lys Gly Gln Trp
 145 150 155

gag aga agg ctt cag aca gat atc aac atg gct aaa caa gct ctt tgt 710
 Glu Arg Arg Leu Gln Thr Asp Ile Asn Met Ala Lys Gln Ala Leu Cys
 160 165 170

gat gcc ttg tct att gac aaa cca caa aac cca act aat ttt tct att 758
 Asp Ala Leu Ser Ile Asp Lys Pro Gln Asn Pro Thr Asn Phe Ser Ile
 175 180 185

ccc gat ctt ggt tat ggt cca tca tct tct tcg tcc tct acc acc acc 806
 Pro Asp Leu Gly Tyr Gly Pro Ser Ser Ser Ser Ser Ser Thr Thr Thr
 190 195 200

acc acc acc acc acc acc acg aga aac act aat cca tac cca tct ggg 854
 Thr Thr Thr Thr Thr Thr Thr Arg Asn Thr Asn Pro Tyr Pro Ser Gly
 205 210 215 220

gtc tat gct tca agt gct gag aac att gct cgt ttg ctt cag aat ttt 902
 Val Tyr Ala Ser Ser Ala Glu Asn Ile Ala Arg Leu Leu Gln Asn Phe
 225 230 235

atg aaa gac aca cca aag acc tcg gtg ccc ttg ccg gtt gca gcc acc 950
 Met Lys Asp Thr Pro Lys Thr Ser Val Pro Leu Pro Val Ala Ala Thr
 240 245 250

gag atg gct atc acc acg gca gct tcg agc cct agc aca acc gaa gga 998
 Glu Met Ala Ile Thr Thr Ala Ala Ser Ser Pro Ser Thr Thr Glu Gly
 255 260 265

gac gga gaa ggg att gac cat tct ttg ttc agc ttc aac tcc ata gat 1046
 Asp Gly Glu Gly Ile Asp His Ser Leu Phe Ser Phe Asn Ser Ile Asp
 270 275 280

gaa gct gaa gag aag cct aaa cta ata gac cat gac att aat ggt cta 1094
 Glu Ala Glu Glu Lys Pro Lys Leu Ile Asp His Asp Ile Asn Gly Leu
 285 290 295 300

att aca caa ggc tct ctt tct ttg ttc gag aaa tgg ctc ttt gat gag 1142
 Ile Thr Gln Gly Ser Leu Ser Leu Phe Glu Lys Trp Leu Phe Asp Glu
 305 310 315

caa agc cac gat atg atc atc aat aac atg tca cta gag ggt cag gaa 1190
 Gln Ser His Asp Met Ile Ile Asn Asn Met Ser Leu Glu Gly Gln Glu
 320 325 330

gtg ttg ttc tagaaagcat taaagtttga cgatttgctt gaggaaccac 1239
 Val Leu Phe
 335

gaggcttagt tataaacaat ttgtataatt aagtactctt tagttttgtt ttcaatcctt 1299

attatgatca tattgcagta attagggatt ttagtcttta gtagtaactc ttaagtttta 1359

acacattttt ctctatcttt ttagtagtaa ctctttatct tttccttaaa tctttgtcga 1419

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<211> 335

<212> PRT

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Gly Pro Gly Asn Trp Arg Ser Val Pro Thr His Thr Gly Leu Arg Arg
 35 40 45

Cys Ser Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro Gly
 50 55 60

Ile Lys Arg Gly Asn Phe Thr Glu His Glu Glu Lys Met Ile Leu His
 65 70 75 80

Leu Gln Ala Leu Leu Gly Asn Arg Trp Ala Ala Ile Ala Ser Tyr Leu
 85 90 95

Pro Glu Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr His Leu
 100 105 110

Lys Lys Lys Leu Lys Lys Met Asn Asp Ser Cys Asp Ser Thr Ile Asn
 115 120 125
 Asn Gly Leu Asp Asn Lys Asp Phe Ser Ile Ser Asn Lys Asn Thr Thr
 130 135 140
 Ser His Gln Ser Ser Asn Ser Ser Lys Gly Gln Trp Glu Arg Arg Leu
 145 150 155 160
 Gln Thr Asp Ile Asn Met Ala Lys Gln Ala Leu Cys Asp Ala Leu Ser
 165 170 175
 Ile Asp Lys Pro Gln Asn Pro Thr Asn Phe Ser Ile Pro Asp Leu Gly
 180 185 190
 Tyr Gly Pro Ser Ser Ser Ser Ser Ser Thr Thr Thr Thr Thr Thr Thr
 195 200 205
 Thr Thr Thr Arg Asn Thr Asn Pro Tyr Pro Ser Gly Val Tyr Ala Ser
 210 215 220
 Ser Ala Glu Asn Ile Ala Arg Leu Leu Gln Asn Phe Met Lys Asp Thr
 225 230 235 240
 Pro Lys Thr Ser Val Pro Leu Pro Val Ala Ala Thr Glu Met Ala Ile
 245 250 255
 Thr Thr Ala Ala Ser Ser Pro Ser Thr Thr Glu Gly Asp Gly Glu Gly
 260 265 270
 Ile Asp His Ser Leu Phe Ser Phe Asn Ser Ile Asp Glu Ala Glu Glu
 275 280 285
 Lys Pro Lys Leu Ile Asp His Asp Ile Asn Gly Leu Ile Thr Gln Gly
 290 295 300
 Ser Leu Ser Leu Phe Glu Lys Trp Leu Phe Asp Glu Gln Ser His Asp
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 325 330 335

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 <222> (180)..(914)
 <223> G994

<220>
 <223> "n" at various positions throughout the sequence
 may be A, T, C, G, other or unknown

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 ttcaaatacca ataaagtttt aatttgatga agcttttttt aaaccatata atataaata 179
 atg ggt ggt cgt aaa cca tgt tgt gat gag gtt gga tta aga aag ggt 227
 Met Gly Gly Arg Lys Pro Cys Cys Asp Glu Val Gly Leu Arg Lys Gly
 1 5 10 15
 cca tgg aca gtg gaa gaa gat ggg aaa cta gtt gat ttc tta agg gca 275
 Pro Trp Thr Val Glu Glu Asp Gly Lys Leu Val Asp Phe Leu Arg Ala
 20 25 30
 cgt ggc aac tgc ggt ggt ggt gga gga gga tgg tgc tgg aga gac gtg 323
 Arg Gly Asn Cys Gly Gly Gly Gly Gly Gly Trp Cys Trp Arg Asp Val
 35 40 45
 cca aaa ctg gcg ggg cta agg agg tgt ggc aaa agt tgc cgt ctc cgg 371
 Pro Lys Leu Ala Gly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg
 50 55 60
 tgg act aat tat ctc cgg cca gat ctc aag aga ggt ctt ttt act gaa 419
 Trp Thr Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Leu Phe Thr Glu
 65 70 75 80
 gaa gaa atc caa cta gtc att gat ctt cat gct cgc ctt ggc aat aga 467
 Glu Glu Ile Gln Leu Val Ile Asp Leu His Ala Arg Leu Gly Asn Arg
 85 90 95
 tgg tcg aag att gca gtg gag tta cca gga aga aca gac aac gat atc 515
 Trp Ser Lys Ile Ala Val Glu Leu Pro Gly Arg Thr Asp Asn Asp Ile
 100 105 110
 aaa aat tat tgg aac act cat ata aag agg aag ctt ata aga atg ggt 563
 Lys Asn Tyr Trp Asn Thr His Ile Lys Arg Lys Leu Ile Arg Met Gly
 115 120 125
 att gat cca aac aca cat cgt cga ttt gac caa caa aaa gtc aac gag 611
 Ile Asp Pro Asn Thr His Arg Arg Phe Asp Gln Gln Lys Val Asn Glu
 130 135 140
 gag gaa acg ata ttg gtc aac gat cca aag cct ctg tct gag acc gag 659
 Glu Glu Thr Ile Leu Val Asn Asp Pro Lys Pro Leu Ser Glu Thr Glu
 145 150 155 160
 gta tct gtt gct ttg aag aat gac acg tca gca gtg tta tca gga aat 707
 Val Ser Val Ala Leu Lys Asn Asp Thr Ser Ala Val Leu Ser Gly Asn
 165 170 175
 cta aac caa ttg gct gac gtg gac ggt gat gat cag ccg tgg agc ttt 755
 Leu Asn Gln Leu Ala Asp Val Asp Gly Asp Asp Gln Pro Trp Ser Phe
 180 185 190
 cta atg gaa aat gac gaa gga gga ggt ggc gac gcc gcc gga gag ctt 803
 Leu Met Glu Asn Asp Glu Gly Gly Gly Gly Asp Ala Ala Gly Glu Leu
 195 200 205

acg atg cta ttg tcc ggt gac att acg tca tca tgt tct tct tcg tca 851
 Thr Met Leu Leu Ser Gly Asp Ile Thr Ser Ser Cys Ser Ser Ser Ser
 210 215 220

tct ttg tgg atg aag tat gga gaa ttc gga tac gaa gat tta gaa ctt 899
 Ser Leu Trp Met Lys Tyr Gly Glu Phe Gly Tyr Glu Asp Leu Glu Leu
 225 230 235 240

gga tgt ttc gat gtt tagagattca agtatgttta attaggccgt aggttgatta 954
 Gly Cys Phe Asp Val
 245

atcataaggt tcattgactt cattctagaa ttgtgtagtt ggaccagtat aaagaatcaa 1014

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aaaaaaaaa a 1095

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Arg Gly Asn Cys Gly Gly Gly Gly Gly Gly Trp Cys Trp Arg Asp Val
 35 40 45

Pro Lys Leu Ala Gly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg
 50 55 60

Trp Thr Asn Tyr Leu Arg Pro Asp Leu Lys Arg Gly Leu Phe Thr Glu
 65 70 75 80

Glu Glu Ile Gln Leu Val Ile Asp Leu His Ala Arg Leu Gly Asn Arg
 85 90 95

Trp Ser Lys Ile Ala Val Glu Leu Pro Gly Arg Thr Asp Asn Asp Ile
 100 105 110

Lys Asn Tyr Trp Asn Thr His Ile Lys Arg Lys Leu Ile Arg Met Gly
 115 120 125

Ile Asp Pro Asn Thr His Arg Arg Phe Asp Gln Gln Lys Val Asn Glu
 130 135 140

Glu Glu Thr Ile Leu Val Asn Asp Pro Lys Pro Leu Ser Glu Thr Glu
 145 150 155 160

Val Ser Val Ala Leu Lys Asn Asp Thr Ser Ala Val Leu Ser Gly Asn
 165 170 175

Leu Asn Gln Leu Ala Asp Val Asp Gly Asp Asp Gln Pro Trp Ser Phe
 180 185 190

Leu Met Glu Asn Asp Glu Gly Gly Gly Gly Asp Ala Ala Gly Glu Leu
 195 200 205

Thr Met Leu Leu Ser Gly Asp Ile Thr Ser Ser Cys Ser Ser Ser Ser
 210 215 220

Ser Leu Trp Met Lys Tyr Gly Glu Phe Gly Tyr Glu Asp Leu Glu Leu
 225 230 235 240

Gly Cys Phe Asp Val
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 <222> (119)..(1126)
 <223> G996

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atg gga aga cat tca tgt tgt tac aaa cag aaa ctg agg aaa gga ctt 166
 Met Gly Arg His Ser Cys Cys Tyr Lys Gln Lys Leu Arg Lys Gly Leu
 1 5 10 15

tgg tct cct gaa gaa gat gag aag ctt ctt cgt tac atc act aag tat 214
 Trp Ser Pro Glu Glu Asp Glu Lys Leu Leu Arg Tyr Ile Thr Lys Tyr
 20 25 30

ggg cat ggt tgc tgg agc tct gtc cct aaa caa gct ggt tta cag aga 262
 Gly His Gly Cys Trp Ser Ser Val Pro Lys Gln Ala Gly Leu Gln Arg
 35 40 45

tgt gga aaa agt tgt aga tta aga tgg ata aat tat tta aga cca gat 310
 Cys Gly Lys Ser Cys Arg Leu Arg Trp Ile Asn Tyr Leu Arg Pro Asp
 50 55 60

ttg aag aga gga gca ttt tct caa gat gaa gaa aat ctc att att gaa 358
 Leu Lys Arg Gly Ala Phe Ser Gln Asp Glu Glu Asn Leu Ile Ile Glu
 65 70 75 80

ctt cat gcc gtt ctt ggc aat aga tgg tct cag ata gct gca cag ctt 406
 Leu His Ala Val Leu Gly Asn Arg Trp Ser Gln Ile Ala Ala Gln Leu
 85 90 95

cct gga aga acc gac aat gaa atc aag aat ctt tgg aat tct tgt ttg	454
Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Leu Trp Asn Ser Cys Leu	
100 105 110	
aag aag aaa ttg agg ctg aga gga att gac ccg gtt aca cac aag ctc	502
Lys Lys Lys Leu Arg Leu Arg Gly Ile Asp Pro Val Thr His Lys Leu	
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tta acc gaa atc gaa acc ggt aca gat gac aaa aca aaa ccg gtt gag	550
Leu Thr Glu Ile Glu Thr Gly Thr Asp Asp Lys Thr Lys Pro Val Glu	
130 135 140	
aag agt caa cag acc tac ctc gtt gag act gat ggc tcc tct agt acc	598
Lys Ser Gln Gln Thr Tyr Leu Val Glu Thr Asp Gly Ser Ser Ser Thr	
145 150 155 160	
act act tgt agt act aac caa aac aac aac act gat cat ctt tat acc	646
Thr Thr Cys Ser Thr Asn Gln Asn Asn Asn Thr Asp His Leu Tyr Thr	
165 170 175	
gga aat ttc ggt ttt caa cgg tta agt cta gaa aac ggt tca aga atc	694
Gly Asn Phe Gly Phe Gln Arg Leu Ser Leu Glu Asn Gly Ser Arg Ile	
180 185 190	
gca gcc ggt tct gac ctc ggt atc tgg att ccc caa acc gga aga aac	742
Ala Ala Gly Ser Asp Leu Gly Ile Trp Ile Pro Gln Thr Gly Arg Asn	
195 200 205	
cat cat cat cat gtc gat gaa acc atc cct agt gca gtg gta cta ccc	790
His His His His Val Asp Glu Thr Ile Pro Ser Ala Val Val Leu Pro	
210 215 220	
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Gly Ser Met Phe Ser Ser Gly Leu Thr Gly Tyr Arg Ser Ser Asn Leu	
225 230 235 240	
ggt tta att gaa ttg gaa aac tca ttc tca acc ggg cca atg atg aca	886
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gag cat cag caa att caa gag agt aac tac aac aat tca aca ttc ttt	934
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Pro Phe Thr Ile Ser Asn His Ser Asn Ser Ser Leu Tyr Ser Asp Ile	
290 295 300	
aaa tca gag acc aat ttt ttt ggc aca gag gct aca aat gtt ggt atg	1078
Lys Ser Glu Thr Asn Phe Phe Gly Thr Glu Ala Thr Asn Val Gly Met	
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 35 40 45

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 50 55 60

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 65 70 75 80

Leu His Ala Val Leu Gly Asn Arg Trp Ser Gln Ile Ala Ala Gln Leu
 85 90 95

Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Leu Trp Asn Ser Cys Leu
 100 105 110

Lys Lys Lys Leu Arg Leu Arg Gly Ile Asp Pro Val Thr His Lys Leu
 115 120 125

Leu Thr Glu Ile Glu Thr Gly Thr Asp Asp Lys Thr Lys Pro Val Glu
 130 135 140

Lys Ser Gln Gln Thr Tyr Leu Val Glu Thr Asp Gly Ser Ser Ser Thr
 145 150 155 160

Thr Thr Cys Ser Thr Asn Gln Asn Asn Asn Thr Asp His Leu Tyr Thr
 165 170 175

Gly Asn Phe Gly Phe Gln Arg Leu Ser Leu Glu Asn Gly Ser Arg Ile
 180 185 190

Ala Ala Gly Ser Asp Leu Gly Ile Trp Ile Pro Gln Thr Gly Arg Asn
 195 200 205

His His His His Val Asp Glu Thr Ile Pro Ser Ala Val Val Leu Pro
 210 215 220

Gly Ser Met Phe Ser Ser Gly Leu Thr Gly Tyr Arg Ser Ser Asn Leu
225 230 235 240

Gly Leu Ile Glu Leu Glu Asn Ser Phe Ser Thr Gly Pro Met Met Thr
245 250 255

Glu His Gln Gln Ile Gln Glu Ser Asn Tyr Asn Asn Ser Thr Phe Phe
260 265 270

Gly Asn Gly Asn Leu Asn Trp Gly Leu Thr Met Glu Glu Asn Gln Asn
275 280 285

Pro Phe Thr Ile Ser Asn His Ser Asn Ser Ser Leu Tyr Ser Asp Ile
290 295 300

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Met Ala Ser Ser Ser Met Ser Thr Ser Ser Trp Thr Ala Arg

1

5

10

gag gac aag caa ttc gaa atg gcg ttg gcg aaa ttc gac aag gac act 159

Glu Asp Lys Gln Phe Glu Met Ala Leu Ala Lys Phe Asp Lys Asp Thr

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cct gac cgt tgg caa aaa att gca agg gca gtt ggt ggg aaa tca act 207

Pro Asp Arg Trp Gln Lys Ile Ala Arg Ala Val Gly Gly Lys Ser Thr

35

40

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Glu Glu Val Lys Arg His Tyr Glu Leu Leu Leu Arg Asp Val Asn Asp

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55

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att gag tca gga cgc tat cca caa cct agg tac cgt aac act aat 300

Ile Glu Ser Gly Arg Tyr Pro Gln Pro Arg Tyr Arg Asn Thr Asn

65

70

75

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 Met Gly Arg Ser Pro Cys Cys Glu Lys Lys Asn Gly Leu Lys
 1 5 10
 aaa gga cca tgg act cct gag gag gat caa aag ctc att gat tat atc 156
 Lys Gly Pro Trp Thr Pro Glu Glu Asp Gln Lys Leu Ile Asp Tyr Ile
 15 20 25 30
 aat ata cat ggt tat gga aat tgg aga act ctt ccc aag aat gct ggg 204
 Asn Ile His Gly Tyr Gly Asn Trp Arg Thr Leu Pro Lys Asn Ala Gly
 35 40 45

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Ser	Ile	Tyr	Asn	Ser	Ser	His	His	His	His	His	His	His	Gln	Gln	His	
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Gln	Ser	Trp	Phe	Pro	Ile	Met	Asp	Gln	Phe	Thr	Asn	Phe	Gln	Asp	Leu	
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atg	cca	atg	aag	acg	acg	gtc	caa	aat	tca	ttg	tca	tac	gat	gat	gat	828
Met	Pro	Met	Lys	Thr	Thr	Val	Gln	Asn	Ser	Leu	Ser	Tyr	Asp	Asp	Asp	
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Cys	Ser	Lys	Ser	Asn	Phe	Val	Leu	Glu	Pro	Tyr	Tyr	Ser	Asp	Phe	Ala	
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 275 280 285

tcc tca act tac atc aat agt agc act tgc agc acc gag gat gaa aaa 972
 Ser Ser Thr Tyr Ile Asn Ser Ser Thr Cys Ser Thr Glu Asp Glu Lys
 290 295 300

gag agt tat tac agt gat aat atc act aat tat tcg ttt gat gtt aat 1020
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 305 310 315

ggt ttt ctc caa ttc caa taaacaaaac gccattggaa tagagttatg 1068
 Gly Phe Leu Gln Phe Gln
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 35 40 45

Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Thr Asn Tyr Leu Arg Pro
 50 55 60

Asp Ile Lys Arg Gly Arg Phe Ser Phe Glu Glu Glu Glu Thr Ile Ile
 65 70 75 80

Gln Leu His Ser Ile Met Gly Asn Lys Trp Ser Ala Ile Ala Ala Arg
 85 90 95

Leu Pro Gly Arg Thr Asp Asn Glu Ile Lys Asn Tyr Trp Asn Thr His
 100 105 110

Ile Arg Lys Arg Leu Leu Lys Met Gly Ile Asp Pro Val Thr His Thr
 115 120 125

Pro Arg Leu Asp Leu Leu Asp Ile Ser Ser Ile Leu Ser Ser Ser Ile
 130 135 140

Tyr Asn Ser Ser His His His His His His His Gln Gln His Met Asn
145 150 155 160

Met Ser Arg Leu Met Met Ser Asp Gly Asn His Gln Pro Leu Val Asn
165 170 175

Pro Glu Ile Leu Lys Leu Ala Thr Ser Leu Phe Ser Asn Gln Asn His
180 185 190

Pro Asn Asn Thr His Glu Asn Asn Thr Val Asn Gln Thr Glu Val Asn
195 200 205

Gln Tyr Gln Thr Gly Tyr Asn Met Pro Gly Asn Glu Glu Leu Gln Ser
210 215 220

Trp Phe Pro Ile Met Asp Gln Phe Thr Asn Phe Gln Asp Leu Met Pro
225 230 235 240

Met Lys Thr Thr Val Gln Asn Ser Leu Ser Tyr Asp Asp Asp Cys Ser
245 250 255

Lys Ser Asn Phe Val Leu Glu Pro Tyr Tyr Ser Asp Phe Ala Ser Val
260 265 270

Leu Thr Thr Pro Ser Ser Ser Pro Thr Pro Leu Asn Ser Ser Ser Ser
275 280 285

Thr Tyr Ile Asn Ser Ser Thr Cys Ser Thr Glu Asp Glu Lys Glu Ser
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Glu Ile Lys Lys Ile Glu Asn Ile Asn Ser Arg Gln Val Thr Phe Ser
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Gln	Ile	Leu	Leu	Asn	Gln	Ile	Glu	Arg	Ser	Arg	Ile	Gln	Glu	Lys	Lys	
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Asn	Glu	Glu	His	His	Ser	Asp	Thr	Ser	Leu	Gln	Leu	Gly	Leu	Ser	Ser	
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 Ser Ser Thr Gly Lys Ile Tyr Asp Phe Ser Ser Val Cys Met Glu Gln
 50 55 60
 Ile Leu Ser Arg Tyr Gly Tyr Thr Thr Ala Ser Thr Glu His Lys Gln
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 Gln Arg Glu His Gln Leu Leu Ile Cys Ala Ser His Gly Asn Glu Ala
 85 90 95
 Val Leu Arg Asn Asp Asp Ser Met Lys Gly Glu Leu Glu Arg Leu Gln
 100 105 110
 Leu Ala Ile Glu Arg Leu Lys Gly Lys Glu Leu Glu Gly Met Ser Phe
 115 120 125
 Pro Asp Leu Ile Ser Leu Glu Asn Gln Leu Asn Glu Ser Leu His Ser
 130 135 140
 Val Lys Asp Gln Lys Thr Gln Ile Leu Leu Asn Gln Ile Glu Arg Ser
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may be A, T, C, G, other or unknown

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gag ctt gcg att ctc tgc gat gct gag gtt ggt gtc atc atc ttc tcc 263
Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Val Ile Ile Phe Ser
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Ile Glu Arg Tyr Ser Asp Ala Lys Gly Glu Thr Ser Ser Glu Asn Asp
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Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Val Ile Ile Phe
 35             40             45

Ser Ser Thr Gly Arg Leu Tyr Asp Phe Ser Ser Ser Ser Met Lys Ser
 50             55             60

Val Ile Glu Arg Tyr Ser Asp Ala Lys Gly Glu Thr Ser Ser Glu Asn
 65             70             75             80

Asp Pro Ala Ser Glu Ile Gln Phe Trp Gln Lys Glu Ala Ala Ile Leu
          85             90             95

Lys Arg Gln Leu His Asn Leu Gln Glu Asn His Arg Gln Met Met Gly
 100             105             110

Glu Glu Leu Ser Gly Leu Ser Val Glu Ala Leu Gln Asn Leu Glu Asn
 115             120             125

Gln Leu Glu Leu Ser Leu Arg Gly Val Arg Met Lys Lys Asp Gln Met
 130             135             140

Leu Ile Glu Glu Ile Gln Val Leu Asn Arg Glu Gly Asn Leu Val His
 145             150             155             160

Gln Glu Asn Leu Asp Leu His Lys Lys Val Asn Leu Met His Gln Gln
          165             170             175

Asn Met Glu Leu His Glu Lys Val Ser Glu Val Glu Gly Val Lys Ile
 180             185             190

Ala Asn Lys Asn Ser Leu Leu Thr Asn Gly Leu Asp Met Arg Asp Thr
 195             200             205

Ser Asn Glu His Val His Leu Gln Leu Ser Gln Pro Gln His Asp His
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gttctcgaaa gatccattaa aatcaaaacc taagctctct ctcttgcttc taggggtttt 180

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Ile Ile Phe Ser Ser Thr Gly Lys Leu Phe Glu Phe Cys Ser Ser Ser

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Lys Leu Asp Gln Pro Ser Leu Glu Leu Gln Leu Val Glu Asn Ser Asp

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His Ala Arg Met Ser Lys Glu Ile Ala Asp Lys Ser His Arg Leu Arg

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Gln Met Arg Gly Glu Glu Leu Gln Gly Leu Asp Ile Glu Glu Leu Gln

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Gln Leu Glu Lys Ala Leu Glu Thr Gly Leu Thr Arg Val Ile Glu Thr

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 Asp His Thr Val Arg
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																10
																15
caa gaa gct gca tca caa ggc tta aaa agc atg gaa cac ttg att cgt																154
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																25
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Gln Ile Ser Ala Pro Ala Pro Val Ser Phe Val Gln Ala Asn Gln Gln	
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Ser Val Thr Leu Asp Phe Thr Arg Pro Ser Val Phe Gly Ala Lys Thr	
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Lys Ser Ser Glu Val Val Glu Phe Ala Lys Glu Ser Phe Ser Val Ser	
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Ser Asn Ser Ser Phe Met Ser Ser Ala Ile Thr Gly Asp Gly Ser Val	
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Ser Lys Gly Ser Ser Ile Phe Leu Ala Pro Ala Pro Ala Val Pro Val	
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Thr Ser Ser Gly Lys Pro Pro Leu Ser Gly Leu Pro Tyr Arg Lys Arg	
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Cys Phe Glu His Asp His Ser Glu Gly Phe Ser Gly Lys Ile Ser Gly	
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Lys Arg Thr Val Arg Val Pro Ala Val Ser Ala Lys Ile Ala Asp Ile	
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Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly Gln Lys Pro Ile Lys	
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Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser Thr Phe Arg Gly	
260 265 270	

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 Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu Asp Asp Ser Thr Met
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 Asn Arg Ser Gly His Ala Arg Phe Arg Arg Gly Pro Val His Ser Pro
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 85 90 95
 Thr Gln Ile Ser Ala Pro Ala Pro Val Ser Phe Val Gln Ala Asn Gln
 100 105 110
 Gln Ser Val Thr Leu Asp Phe Thr Arg Pro Ser Val Phe Gly Ala Lys
 115 120 125
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 130 135 140
 Ser Ser Asn Ser Ser Phe Met Ser Ser Ala Ile Thr Gly Asp Gly Ser
 145 150 155 160

Val Ser Lys Gly Ser Ser Ile Phe Leu Ala Pro Ala Pro Ala Val Pro
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 180 185 190
 Arg Cys Phe Glu His Asp His Ser Glu Gly Phe Ser Gly Lys Ile Ser
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 Gly Ser Gly Asn Gly Lys Cys His Cys Lys Lys Ser Arg Lys Asn Arg
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 Met Lys Arg Thr Val Arg Val Pro Ala Val Ser Ala Lys Ile Ala Asp
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 Ile Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly Gln Lys Pro Ile
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 Gly Cys Pro Ala Arg Lys His Val Glu Arg Ala Leu Asp Asp Ser Thr
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 gttcggatca gagcacagtt ggatgttagc gacggaactg aggatttcag tttgcggctg 300
 cggcggctgt gacggtgttt gtgtgtcgtc ttcttttatc aatcaggagt ttcacacag 360

tttgatcaga gattcagcca aattcttggga tactaa															atg	gct	ggt	ttt	gat	gaa	414
															Met	Ala	Gly	Phe	Asp	Glu	
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Asn Val Ala Val Met Gly Glu Trp Val Pro Arg Ser Pro Ser Pro Gly																					
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Thr Leu Phe Ser Ser Ala Ile Gly Glu Glu Lys Ser Ser Lys Arg Val																					
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ctt gaa aga gag tta tct ttg aat cat ggt caa gtt att ggt tta gaa																					558
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Phe Arg Gly Gly Leu Ser Glu Arg Ile Ala Ala Arg Ala Gly Phe Asn																					
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gct cca agg ttg aac act gag aat atc cgc acc aac acc gac ttt tcc																					702
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Val Asn Gly Asn Ala Leu Ser Ser Glu Lys Ala Lys Asp Glu Phe Phe																					
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Asp Asp Ile Gly Ala Ser Phe Ser Phe His Pro Val Ser Arg Ser Ser																					
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aac tac aac aat aga tct tct tct cat caa tcc gca gaa gaa gta aaa																					1038
Asn Tyr Asn Asn Arg Ser Ser Ser His Gln Ser Ala Glu Glu Val Lys																					
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gac aat caa aac ggg cag aac aag aca tct gat gtc act aca aac acc	1134
Asp Asn Gln Asn Gly Gln Asn Lys Thr Ser Asp Val Thr Thr Asn Thr	
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Ser Leu Glu Thr Val Asp His Gln Glu Glu Glu Glu Glu Gln Arg Arg	
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Gly Asp Ser Met Ala Gly Gly Ala Pro Ala Glu Asp Gly Tyr Asn Trp	
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Tyr Tyr Lys Cys Thr Asn Pro Asn Cys Gln Val Lys Lys Lys Val Glu	
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Arg Ser Arg Glu Gly His Ile Thr Glu Ile Ile Tyr Lys Gly Ala His	
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Gln Val Ile Gly Leu Glu Glu Asp Thr Ser Ser Asn His Asn Lys Asp
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Ala Arg Ala Gly Phe Asn Ala Pro Arg Leu Asn Thr Glu Asn Ile Arg
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Thr Asn Thr Asp Phe Ser Ile Asp Ser Asn Leu Arg Ser Pro Cys Leu
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Thr Ile Ser Ser Pro Gly Leu Ser Pro Ala Thr Leu Leu Glu Ser Pro
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Val Phe Leu Ser Asn Pro Leu Ala Gln Pro Ser Pro Thr Thr Gly Lys
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Phe Pro Phe Leu Pro Gly Val Asn Gly Asn Ala Leu Ser Ser Glu Lys
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Ala Lys Asp Glu Phe Phe Asp Asp Ile Gly Ala Ser Phe Ser Phe His
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Pro Val Ser Arg Ser Ser Ser Ser Phe Phe Gln Gly Thr Thr Glu Met
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 Met Ser Val Asp Tyr Gly Asn Tyr Asn Asn Arg Ser Ser Ser His Gln
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 Ser Ala Glu Glu Val Lys Pro Gly Ser Glu Asn Ile Glu Ser Ser Asn
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 225 230 235 240
 Asp Val Thr Thr Asn Thr Ser Leu Glu Thr Val Asp His Gln Glu Glu
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 Glu Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Leu Val Lys Gly
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 Val Lys Lys Lys Val Glu Arg Ser Arg Glu Gly His Ile Thr Glu Ile
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 Ile Tyr Lys Gly Ala His Asn His Leu Lys Pro Pro Pro Asn Arg Arg
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 Gln Gly Gly Ser Asn Glu Asn Asn Val Glu Glu Gly Ser Thr Arg Phe
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 Glu Tyr Gly Asn Gln Ser Gly Ser Ile Gln Ala Gln Thr Gly Gly Gln
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 Ser Asn Asp Glu Asp Glu Asp Asp Arg Gly Thr His Gly Ser Val Ser
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 Leu Gly Tyr Asp Gly Gly Gly Gly Gly Gly Gly Glu Gly Asp Glu
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 Ser Glu Ser Lys Arg Arg Lys Leu Glu Ala Phe Ala Ala Glu Met Ser
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Ser Asp Val Asp Ile Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly
485 490 495

Gln Lys Val Val Lys Gly Asn Pro Asn Pro Arg Ser Tyr Tyr Lys Cys
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Thr Ala Pro Gly Cys Thr Val Arg Lys His Val Glu Arg Ala Ser His
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Asp Leu Lys Ser Val Ile Thr Thr Tyr Glu Gly Lys His Asn His Asp
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Val Pro Ala Ala Arg Asn Ser Ser His Gly Gly Gly Gly Asp Ser Gly
545 550 555 560

Asn Gly Asn Ser Gly Gly Ser Ala Ala Val Ser His His Tyr His Asn
565 570 575

Gly His His Ser Glu Pro Pro Arg Gly Arg Phe Asp Arg Gln Val Thr
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Thr Asn Asn Gln Ser Pro Phe Ser Arg Pro Phe Ser Phe Gln Pro His
595 600 605

Leu Gly Pro Pro Ser Gly Phe Ser Phe Gly Leu Gly Gln Thr Gly Leu
610 615 620

Val Asn Leu Ser Met Pro Gly Leu Ala Tyr Gly Gln Gly Lys Met Pro
625 630 635 640

Gly Leu Pro His Pro Tyr Met Thr Gln Pro Val Gly Met Ser Glu Ala
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<213> Arabidopsis thaliana

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<221> CDS

<222> (197)..(1735)

<223> G878

<220>

<223> "n" at various positions throughout the sequence
may be A, T, C, G, other or unknown

<400> 77

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gagaaacacg acacgaattt tgtataatta agattacaca aaaaaaagtg ttagaaagag 120

aaatatcttc ttcttttttc tgtgtgagtt gggtttgta aagttttatc ctttttgttc 180
 tcaaaatcaa gaatcg atg gcg gag aag gaa gaa aaa gaa cca tcg aag tta 232
 Met Ala Glu Lys Glu Glu Lys Glu Pro Ser Lys Leu
 1 5 10
 aaa tca tcc acc gga gtt tca cgg cca acg att tca cta cct cct cga 280
 Lys Ser Ser Thr Gly Val Ser Arg Pro Thr Ile Ser Leu Pro Pro Arg
 15 20 25
 ccg ttt ggt gaa atg ttt ttt agc ggt ggc gtt gga ttt agt cct gga 328
 Pro Phe Gly Glu Met Phe Phe Ser Gly Gly Val Gly Phe Ser Pro Gly
 30 35 40
 cca atg act ctc gtc tca aat tta ttc tct gat cct gat gag ttc aag 376
 Pro Met Thr Leu Val Ser Asn Leu Phe Ser Asp Pro Asp Glu Phe Lys
 45 50 55 60
 tct ttc tct cag ctt tta gct gga gct atg gct tct ccg gcg gca gct 424
 Ser Phe Ser Gln Leu Leu Ala Gly Ala Met Ala Ser Pro Ala Ala Ala
 65 70 75
 gct gtt gcc gcc gct gct gtg gtt gct act gct cat cat cag aca cct 472
 Ala Val Ala Ala Ala Val Val Ala Thr Ala His His Gln Thr Pro
 80 85 90
 gtg agc tct gtc ggt gat ggc ggt gga agc ggt ggt gat gtt gac ccg 520
 Val Ser Ser Val Gly Asp Gly Gly Gly Ser Gly Gly Asp Val Asp Pro
 95 100 105
 agg ttt aag cag agt aga cca acg gga ttg atg ata act caa cca ccg 568
 Arg Phe Lys Gln Ser Arg Pro Thr Gly Leu Met Ile Thr Gln Pro Pro
 110 115 120
 ggg atg ttt act gta ccg ccg ggg tta agt ccg gct act ctt ttg gat 616
 Gly Met Phe Thr Val Pro Pro Gly Leu Ser Pro Ala Thr Leu Leu Asp
 125 130 135 140
 tct ccg agc ttc ttt ggt ctt ttt tca cct ctt cag gga aca ttt ggt 664
 Ser Pro Ser Phe Phe Gly Leu Phe Ser Pro Leu Gln Gly Thr Phe Gly
 145 150 155
 atg aca cat caa caa gct tta gca caa gtc act gca caa gca gtt caa 712
 Met Thr His Gln Gln Ala Leu Ala Gln Val Thr Ala Gln Ala Val Gln
 160 165 170
 ggc aat aat gtt cat atg cag caa tca caa caa tct gaa tat cct tct 760
 Gly Asn Asn Val His Met Gln Gln Ser Gln Gln Ser Glu Tyr Pro Ser
 175 180 185
 tct aca caa caa caa caa caa caa caa caa gct tca ttg act gag 808
 Ser Thr Gln Gln Gln Gln Gln Gln Gln Gln Ala Ser Leu Thr Glu
 190 195 200
 att cca tca ttt tct tct gca cct agg tct cag att cga gcc tcg gtt 856
 Ile Pro Ser Phe Ser Ser Ala Pro Arg Ser Gln Ile Arg Ala Ser Val
 205 210 215 220

caa gaa aca tcg cag ggt cag aga gag act tcg gaa ata tct gtc ttt	904
Gln Glu Thr Ser Gln Gly Gln Arg Glu Thr Ser Glu Ile Ser Val Phe	
225 230 235	
gag cat cgg tca cag cct caa aat gct gac aaa cca gct gat gat gga	952
Glu His Arg Ser Gln Pro Gln Asn Ala Asp Lys Pro Ala Asp Asp Gly	
240 245 250	
tac aac tgg cgg aaa tat ggg cag aag caa gtg aag ggg agc gat ttt	1000
Tyr Asn Trp Arg Lys Tyr Gly Gln Lys Gln Val Lys Gly Ser Asp Phe	
255 260 265	
cct cgg agt tat tac aaa tgt acg cat cca gct tgt cct gtc aag aag	1048
Pro Arg Ser Tyr Tyr Lys Cys Thr His Pro Ala Cys Pro Val Lys Lys	
270 275 280	
aaa gtg gag agg tca ctc gat gga caa gta acg gaa atc atc tac aag	1096
Lys Val Glu Arg Ser Leu Asp Gly Gln Val Thr Glu Ile Ile Tyr Lys	
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ggg caa cac aat cat gag ctt cct caa aag cgc ggt aac aat aac ggg	1144
Gly Gln His Asn His Glu Leu Pro Gln Lys Arg Gly Asn Asn Asn Gly	
305 310 315	
agt tgt aaa agt tct gat att gca aat cag ttt caa aca agt aat agc	1192
Ser Cys Lys Ser Ser Asp Ile Ala Asn Gln Phe Gln Thr Ser Asn Ser	
320 325 330	
agt ctc aac aag agt aag agg gac cag gaa aca agc caa gtt aca aca	1240
Ser Leu Asn Lys Ser Lys Arg Asp Gln Glu Thr Ser Gln Val Thr Thr	
335 340 345	
aca gag cag atg tct gaa gca agt gat agc gag gag gtt ggg aat gca	1288
Thr Glu Gln Met Ser Glu Ala Ser Asp Ser Glu Glu Val Gly Asn Ala	
350 355 360	
gag act agt gtg gga gaa aga cat gag gat gag cct gat ccc aag cga	1336
Glu Thr Ser Val Gly Glu Arg His Glu Asp Glu Pro Asp Pro Lys Arg	
365 370 375 380	
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Arg Asn Thr Glu Val Arg Val Ser Glu Pro Val Ala Ser Ser His Arg	
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act gtg aca gag cct agg att att gtc caa acg acg agt gaa gtt gac	1432
Thr Val Thr Glu Pro Arg Ile Ile Val Gln Thr Thr Ser Glu Val Asp	
400 405 410	
ctc tta gat gat gga tat agg tgg cgc aag tat ggt cag aaa gta gtc	1480
Leu Leu Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val Val	
415 420 425	
aaa gga aat cct tat ccg agg agc tac tat aag tgt aca aca cca gat	1528
Lys Gly Asn Pro Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr Thr Pro Asp	
430 435 440	

tgc gga gta agg aaa cat gta gag aga gca gca act gac cca aaa gct 1576
 Cys Gly Val Arg Lys His Val Glu Arg Ala Ala Thr Asp Pro Lys Ala
 445 450 455 460

gtt gta aca aca tat gaa ggt aaa cat aac cat gat gtt cca gct gct 1624
 Val Val Thr Thr Tyr Glu Gly Lys His Asn His Asp Val Pro Ala Ala
 465 470 475

aga acc agc agc cat cag tta aga cca aac aat caa cac aac acc tca 1672
 Arg Thr Ser Ser His Gln Leu Arg Pro Asn Asn Gln His Asn Thr Ser
 480 485 490

acg gtt aac ttc aat cat caa cag cct gtt gca cgt tta agg ctt aaa 1720
 Thr Val Asn Phe Asn His Gln Gln Pro Val Ala Arg Leu Arg Leu Lys
 495 500 505

gaa gag caa atc act tgacagagaa gaagaatagc acggcgcttg agcttttgtg 1775
 Glu Glu Gln Ile Thr
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agtttaatga atcttctttt tggtaatga acctgttttt gttgcctcaa aacaccacag 1835

gtttctctgg acagaatctc tgatattaca gtttcaaaag gtatgttctt ttatttcatg 1895

ttggaatctt ctgtgtaatc ttaagaagct ttaggaggtat atgtaaaaaa ccagattcaa 1955

agttatgccc ttatgtgaat tcttttgtac atgggataaa caaaatttac aggtatcctt 2015

tttgttcttg ttgtaaaaaa aaaaaaaaaa 2044

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Met Phe Phe Ser Gly Gly Val Gly Phe Ser Pro Gly Pro Met Thr Leu
 35 40 45

Val Ser Asn Leu Phe Ser Asp Pro Asp Glu Phe Lys Ser Phe Ser Gln
 50 55 60

Leu Leu Ala Gly Ala Met Ala Ser Pro Ala Ala Ala Ala Val Ala Ala
 65 70 75 80

Ala Ala Val Val Ala Thr Ala His His Gln Thr Pro Val Ser Ser Val
 85 90 95

Pro Arg Ile Ile Val Gln Thr Thr Ser Glu Val Asp Leu Leu Asp Asp
 405 410 415

Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val Val Lys Gly Asn Pro
 420 425 430

Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr Thr Pro Asp Cys Gly Val Arg
 435 440 445

Lys His Val Glu Arg Ala Ala Thr Asp Pro Lys Ala Val Val Thr Thr
 450 455 460

Tyr Glu Gly Lys His Asn His Asp Val Pro Ala Ala Arg Thr Ser Ser
 465 470 475 480

His Gln Leu Arg Pro Asn Asn Gln His Asn Thr Ser Thr Val Asn Phe
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Asn His Gln Gln Pro Val Ala Arg Leu Arg Leu Lys Glu Glu Gln Ile
 500 505 510

Thr

<210> 79
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 <223> G883

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atcatc atg gcc gtc gat cta atg cgt ttc cct aag ata gat gat caa 108
 Met Ala Val Asp Leu Met Arg Phe Pro Lys Ile Asp Asp Gln
 1 5 10

acg gct att cag gaa gct gca tcg caa ggt tta caa agt atg gaa cat 156
 Thr Ala Ile Gln Glu Ala Ala Ser Gln Gly Leu Gln Ser Met Glu His
 15 20 25 30

ctg atc cgt gtc ctc tct aac cgt ccc gaa caa caa cac aac gtt gac 204
 Leu Ile Arg Val Leu Ser Asn Arg Pro Glu Gln Gln His Asn Val Asp
 35 40 45

tgc tcc gag atc act gac ttc acc gtt tct aaa ttc aaa acc gtc att 252
 Cys Ser Glu Ile Thr Asp Phe Thr Val Ser Lys Phe Lys Thr Val Ile
 50 55 60

tct ctc ctt aac cgt act ggt cac gct cgg ttc aga cgc gga ccg gtt 300
 Ser Leu Leu Asn Arg Thr Gly His Ala Arg Phe Arg Arg Gly Pro Val
 65 70 75

cac His	tcc Ser 80	act Thr	tcc Ser	tct Ser	gcc Ala	gca Ala 85	tct Ser	cag Gln	aaa Lys	cta Leu	cag Gln 90	agt Ser	cag Gln	atc Ile	gtt Val	348
aaa Lys 95	aat Asn	act Thr	caa Gln	cct Pro	gag Glu 100	gct Ala	ccg Pro	att Ile	gtt Val 105	tct Ser	cag Gln	cca Pro	gtg Val	aga Arg	aca Thr 110	396
act Thr	acg Thr	aat Asn	cac His	cct Pro 115	caa Gln	atc Ile	gtt Val	cct Pro	cca Pro 120	ccg Pro	tct Ser	agt Ser	gta Val	aca Thr 125	ctc Leu	444
gat Asp	ttc Phe	tct Ser	aaa Lys 130	cca Pro	agc Ser	atc Ile	ttc Phe	ggc Gly 135	acc Thr	aaa Lys	gct Ala	aag Lys	agc Ser 140	gcc Ala	gag Glu	492
ctg Leu	gaa Glu	ttc Phe 145	tcc Ser	aaa Lys	gaa Glu	aac Asn 150	ttc Phe	agt Ser	gtt Val	tct Ser	tta Leu	aac Asn 155	tcc Ser	tca Ser	ttc Phe	540
atg Met	tcg Ser 160	tcg Ser	gcg Ala	ata Ile	acc Thr	gga Gly 165	gac Asp	ggc Gly	agc Ser	gtc Val	tcc Ser 170	aat Asn	gga Gly	aaa Lys	atc Ile	588
ttc Phe 175	ctt Leu	gct Ala	tct Ser	gct Ala	ccg Pro 180	tcg Ser	cag Gln	cct Pro	gtt Val 185	aac Asn	tct Ser	tcc Ser	gga Gly	aaa Lys	cca Pro 190	636
ccg Pro	ttg Leu	gct Ala	ggt Gly	cat His 195	cct Pro	tac Tyr	aga Arg	aag Lys	aga Arg 200	tgt Cys	ctc Leu	gag Glu	cat His	gag Glu 205	cac His	684
tca Ser	gag Glu	agt Ser	ttc Phe 210	tcc Ser	gga Gly	aaa Lys	gtc Val	tcc Ser 215	ggc Gly	tcc Ser	gcc Ala	tac Tyr	gga Gly 220	aag Lys	tgc Cys	732
cat His	tgc Cys	aag Lys 225	aaa Lys	agg Arg	aaa Lys	aat Asn	cgg Arg 230	atg Met	aag Lys	aga Arg	acc Thr 235	gtg Val	aga Arg	gta Val	ccg Pro	780
gcg Ala	ata Ile 240	agt Ser	gca Ala	aag Lys	atc Ile	gcc Ala 245	gat Asp	att Ile	cca Pro	ccg Pro	gac Asp 250	gaa Glu	tat Tyr	tcg Ser	tgg Trp	828
agg Arg 255	aag Lys	tac Tyr	gga Gly	caa Gln	aaa Lys 260	ccg Pro	atc Ile	aag Lys	ggc Gly	tca Ser 265	cca Pro	cac His	cca Pro	cgt Arg	ggt Gly 270	876
tac Tyr	tac Tyr	aag Lys	tgc Cys	agt Ser 275	aca Thr	ttc Phe	aga Arg	gga Gly	tgt Cys 280	cca Pro	gcg Ala	agg Arg	aaa Lys	cac His 285	gtg Val	924
gaa Glu	cga Arg	gca Ala	tta Leu 290	gat Asp	gat Asp	cca Pro	gcg Ala	atg Met 295	ctt Leu	att Ile	gtg Val	aca Thr	tac Tyr	gaa Glu	gga Gly	972

gag cac cgt cat aac caa tcc gcg atg cag gag aat att tct tct tca 1020
 Glu His Arg His Asn Gln Ser Ala Met Gln Glu Asn Ile Ser Ser Ser
 305 310 315

ggc att aat gat tta gtg ttt gcc tcg gct tgactttttt ttgtactatt 1070
 Gly Ile Asn Asp Leu Val Phe Ala Ser Ala
 320 325

tgttttttga ttttttgagt acttttagatg gattgaaatt tgtaaatttt tttattaaga 1130

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<210> 80

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<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G883

<400> 80

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Arg Val Leu Ser Asn Arg Pro Glu Gln Gln His Asn Val Asp Cys Ser
 35 40 45

Glu Ile Thr Asp Phe Thr Val Ser Lys Phe Lys Thr Val Ile Ser Leu
 50 55 60

Leu Asn Arg Thr Gly His Ala Arg Phe Arg Arg Gly Pro Val His Ser
 65 70 75 80

Thr Ser Ser Ala Ala Ser Gln Lys Leu Gln Ser Gln Ile Val Lys Asn
 85 90 95

Thr Gln Pro Glu Ala Pro Ile Val Ser Gln Pro Val Arg Thr Thr Thr
 100 105 110

Asn His Pro Gln Ile Val Pro Pro Pro Ser Ser Val Thr Leu Asp Phe
 115 120 125

Ser Lys Pro Ser Ile Phe Gly Thr Lys Ala Lys Ser Ala Glu Leu Glu
 130 135 140

Phe Ser Lys Glu Asn Phe Ser Val Ser Leu Asn Ser Ser Phe Met Ser
 145 150 155 160

Ser Ala Ile Thr Gly Asp Gly Ser Val Ser Asn Gly Lys Ile Phe Leu
 165 170 175

agt cct ggt ccg atg act ctg gtc tct aat atg ttc cct gat toc gat 198
 Ser Pro Gly Pro Met Thr Leu Val Ser Asn Met Phe Pro Asp Ser Asp
 45 50 55

gag ttt agg tct ttc tct cag ctt ctc gct gga gcc atg tct tct cca	246
Glu Phe Arg Ser Phe Ser Gln Leu Leu Ala Gly Ala Met Ser Ser Pro	
60 65 70	
gcg act gca gct gct gct gct gct gct gcg acg gct agt gat tac cag	294
Ala Thr Ala Ala Ala Ala Ala Ala Ala Ala Thr Ala Ser Asp Tyr Gln	
75 80 85	
aga ctt ggt gaa ggg act aat agc tct agt ggt gat gtt gac ccg aga	342
Arg Leu Gly Glu Gly Thr Asn Ser Ser Ser Gly Asp Val Asp Pro Arg	
90 95 100	
ttc aag caa aac aga cca acc ggt ttg atg att tct caa tct caa tcg	390
Phe Lys Gln Asn Arg Pro Thr Gly Leu Met Ile Ser Gln Ser Gln Ser	
105 110 115 120	
ccg tcg atg ttc acc gta ccg cct ggt tta agt cca gct atg ttg ctc	438
Pro Ser Met Phe Thr Val Pro Pro Gly Leu Ser Pro Ala Met Leu Leu	
125 130 135	
gat tca cca agc ttt ttg ggt ctt ttc tct ccc gtt cag gga tca tat	486
Asp Ser Pro Ser Phe Leu Gly Leu Phe Ser Pro Val Gln Gly Ser Tyr	
140 145 150	
gga atg aca cat cag caa gct cta gct caa gtc act gct caa gca gtt	534
Gly Met Thr His Gln Gln Ala Leu Ala Gln Val Thr Ala Gln Ala Val	
155 160 165	
caa gcc aat gcc aat atg caa cca caa aca gag tac cct cct ccc tct	582
Gln Ala Asn Ala Asn Met Gln Pro Gln Thr Glu Tyr Pro Pro Pro Ser	
170 175 180	
caa gtt caa tca ttt tca tcg ggt caa gcg cag atc ccg acc tcg gct	630
Gln Val Gln Ser Phe Ser Ser Gly Gln Ala Gln Ile Pro Thr Ser Ala	
185 190 195 200	
cca cta cca gct caa aga gaa acc tca gat gta acc atc ata gag cac	678
Pro Leu Pro Ala Gln Arg Glu Thr Ser Asp Val Thr Ile Ile Glu His	
205 210 215	
agg tca caa cag cct cta aat gtt gac aaa cca gct gat gat ggc tat	726
Arg Ser Gln Gln Pro Leu Asn Val Asp Lys Pro Ala Asp Asp Gly Tyr	
220 225 230	
aac tgg cga aaa tat ggg caa aag caa gtt aaa ggt agc gag ttt cca	774
Asn Trp Arg Lys Tyr Gly Gln Lys Gln Val Lys Gly Ser Glu Phe Pro	
235 240 245	
cga agc tat tac aag tgt act aat cca gga tgt cct gtc aag aag aag	822
Arg Ser Tyr Tyr Lys Cys Thr Asn Pro Gly Cys Pro Val Lys Lys Lys	
250 255 260	
gtt gag aga tct ctt gat gga caa gta acg gag att atc tac aaa ggt	870
Val Glu Arg Ser Leu Asp Gly Gln Val Thr Glu Ile Ile Tyr Lys Gly	
265 270 275 280	

cag cac aat cat gaa cct cct caa aac act aag cga ggt aac aaa gat	918
Gln His Asn His Glu Pro Pro Gln Asn Thr Lys Arg Gly Asn Lys Asp	
285 290 295	
aac acc gcg aat ata aat ggg agt tcg ata aat aac aat cgc ggg agt	966
Asn Thr Ala Asn Ile Asn Gly Ser Ser Ile Asn Asn Asn Arg Gly Ser	
300 305 310	
tct gaa ttg ggg gca tca cag ttt caa act aat agc tcc aac aag act	1014
Ser Glu Leu Gly Ala Ser Gln Phe Gln Thr Asn Ser Ser Asn Lys Thr	
315 320 325	
aag aga gag caa cat gaa gca gta agt caa gct acg aca aca gag cac	1062
Lys Arg Glu Gln His Glu Ala Val Ser Gln Ala Thr Thr Thr Glu His	
330 335 340	
ttg tct gag gca agt gac ggt gaa gaa gtt ggt aat gga gaa act gat	1110
Leu Ser Glu Ala Ser Asp Gly Glu Glu Val Gly Asn Gly Glu Thr Asp	
345 350 355 360	
gtg aga gag aaa gat gag aat gag cct gat ccc aag aga aga agt aca	1158
Val Arg Glu Lys Asp Glu Asn Glu Pro Asp Pro Lys Arg Arg Ser Thr	
365 370 375	
gaa gtt cgg att tca gaa cca gct cct gct gct tca cat aga act gtg	1206
Glu Val Arg Ile Ser Glu Pro Ala Pro Ala Ala Ser His Arg Thr Val	
380 385 390	
aca gag cct aga att att gtc caa acg acg agt gaa gtt gat ctt cta	1254
Thr Glu Pro Arg Ile Ile Val Gln Thr Thr Ser Glu Val Asp Leu Leu	
395 400 405	
gat gat gga tat agg tgg cgt aaa tat gga cag aaa gtt gtc aaa ggg	1302
Asp Asp Gly Tyr Arg Trp Arg Lys Tyr Gly Gln Lys Val Val Lys Gly	
410 415 420	
aat cct tat ccg agg agc tac tac aag tgc aca aca cca gga tgt ggt	1350
Asn Pro Tyr Pro Arg Ser Tyr Tyr Lys Cys Thr Thr Pro Gly Cys Gly	
425 430 435 440	
gtg agg aaa cat gta gag aga gca gca aca gat cca aaa gct gta gta	1398
Val Arg Lys His Val Glu Arg Ala Ala Thr Asp Pro Lys Ala Val Val	
445 450 455	
aca aca tat gaa gga aaa cat aac cat gac ctt ccc gct gct aaa tca	1446
Thr Thr Tyr Glu Gly Lys His Asn His Asp Leu Pro Ala Ala Lys Ser	
460 465 470	
agc agc cat gcc gct gca gcg gca cag tta agg cca gat aat cga cct	1494
Ser Ser His Ala Ala Ala Ala Gln Leu Arg Pro Asp Asn Arg Pro	
475 480 485	
ggc ggt ttg gct aac tta aat caa cag cag cag caa cag ccc gtt gcg	1542
Gly Gly Leu Ala Asn Leu Asn Gln Gln Gln Gln Gln Gln Pro Val Ala	
490 495 500	

cgg cta agg ctt aaa gaa gag caa aca act tgagagaaga aaactcttga 1592
 Arg Leu Arg Leu Lys Glu Glu Gln Thr Thr
 505 510

ccgttttttca ttacaaaagc tttcaaattc cactcacaca cttgtctgaa aaatctagca 1652
 gtttgcagga aagaaacagc ttcaagaggt tgtagttctt ctatgttctg gtgtaaaact 1712
 taaaagcttt ttaggggtttt cagatttctg tttactaata ctgtatgtga attcttttgt 1772
 acatgaggaa gaaaattaca gggggatatt ttgtgttgta tcttttgtgt tattgtttca 1832
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<220>
 <223> G884

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 Phe Phe Asn Gly Gly Val Gly Phe Ser Pro Gly Pro Met Thr Leu Val
 35 40 45
 Ser Asn Met Phe Pro Asp Ser Asp Glu Phe Arg Ser Phe Ser Gln Leu
 50 55 60
 Leu Ala Gly Ala Met Ser Ser Pro Ala Thr Ala Ala Ala Ala Ala
 65 70 75 80
 Ala Ala Thr Ala Ser Asp Tyr Gln Arg Leu Gly Glu Gly Thr Asn Ser
 85 90 95
 Ser Ser Gly Asp Val Asp Pro Arg Phe Lys Gln Asn Arg Pro Thr Gly
 100 105 110
 Leu Met Ile Ser Gln Ser Gln Ser Pro Ser Met Phe Thr Val Pro Pro
 115 120 125
 Gly Leu Ser Pro Ala Met Leu Leu Asp Ser Pro Ser Phe Leu Gly Leu
 130 135 140
 Phe Ser Pro Val Gln Gly Ser Tyr Gly Met Thr His Gln Gln Ala Leu
 145 150 155 160
 Ala Gln Val Thr Ala Gln Ala Val Gln Ala Asn Ala Asn Met Gln Pro
 165 170 175

Gln Thr Glu Tyr Pro Pro Pro Ser Gln Val Gln Ser Phe Ser Ser Gly
 180 185 190
 Gln Ala Gln Ile Pro Thr Ser Ala Pro Leu Pro Ala Gln Arg Glu Thr
 195 200 205
 Ser Asp Val Thr Ile Ile Glu His Arg Ser Gln Gln Pro Leu Asn Val
 210 215 220
 Asp Lys Pro Ala Asp Asp Gly Tyr Asn Trp Arg Lys Tyr Gly Gln Lys
 225 230 235 240
 Gln Val Lys Gly Ser Glu Phe Pro Arg Ser Tyr Tyr Lys Cys Thr Asn
 245 250 255
 Pro Gly Cys Pro Val Lys Lys Lys Val Glu Arg Ser Leu Asp Gly Gln
 260 265 270
 Val Thr Glu Ile Ile Tyr Lys Gly Gln His Asn His Glu Pro Pro Gln
 275 280 285
 Asn Thr Lys Arg Gly Asn Lys Asp Asn Thr Ala Asn Ile Asn Gly Ser
 290 295 300
 Ser Ile Asn Asn Asn Arg Gly Ser Ser Glu Leu Gly Ala Ser Gln Phe
 305 310 315 320
 Gln Thr Asn Ser Ser Asn Lys Thr Lys Arg Glu Gln His Glu Ala Val
 325 330 335
 Ser Gln Ala Thr Thr Thr Glu His Leu Ser Glu Ala Ser Asp Gly Glu
 340 345 350
 Glu Val Gly Asn Gly Glu Thr Asp Val Arg Glu Lys Asp Glu Asn Glu
 355 360 365
 Pro Asp Pro Lys Arg Arg Ser Thr Glu Val Arg Ile Ser Glu Pro Ala
 370 375 380
 Pro Ala Ala Ser His Arg Thr Val Thr Glu Pro Arg Ile Ile Val Gln
 385 390 395 400
 Thr Thr Ser Glu Val Asp Leu Leu Asp Asp Gly Tyr Arg Trp Arg Lys
 405 410 415
 Tyr Gly Gln Lys Val Val Lys Gly Asn Pro Tyr Pro Arg Ser Tyr Tyr
 420 425 430
 Lys Cys Thr Thr Pro Gly Cys Gly Val Arg Lys His Val Glu Arg Ala
 435 440 445
 Ala Thr Asp Pro Lys Ala Val Val Thr Thr Tyr Glu Gly Lys His Asn
 450 455 460
 His Asp Leu Pro Ala Ala Lys Ser Ser Ser His Ala Ala Ala Ala Ala
 465 470 475 480

66
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Gln Leu Arg Pro Asp Asn Arg Pro Gly Gly Leu Ala Asn Leu Asn Gln
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Gln Gln Gln Gln Gln Pro Val Ala Arg Leu Arg Leu Lys Glu Glu Gln
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Thr Thr

<210> 83

<211> 1296

<212> DNA

<213> Arabidopsis thaliana

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<222> (114)..(1151)

<223> G920

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 Met
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gat tcg aat agt aac aac acg aaa tcc ata aag aga aaa gtt gtc gac 164
 Asp Ser Asn Ser Asn Asn Thr Lys Ser Ile Lys Arg Lys Val Val Asp
 5 10 15

caa ctt gtc gaa ggc tat gaa ttc gct act cag ctt cag ctt ctc ctt 212
 Gln Leu Val Glu Gly Tyr Glu Phe Ala Thr Gln Leu Gln Leu Leu Leu
 20 25 30

tct cat caa cac tct aac cag tac cac atc gat gag acc cgt ctt gtt 260
 Ser His Gln His Ser Asn Gln Tyr His Ile Asp Glu Thr Arg Leu Val
 35 40 45

tcc ggg tcg ggt tca gtt tcc ggt ggt cca gat ccc gtt gat gag ctc 308
 Ser Gly Ser Gly Ser Val Ser Gly Gly Pro Asp Pro Val Asp Glu Leu
 50 55 60 65

atg tct aag atc ttg gga tct ttc cat aaa act ata tcg gtt ctt gat 356
 Met Ser Lys Ile Leu Gly Ser Phe His Lys Thr Ile Ser Val Leu Asp
 70 75 80

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 caa aag gag att ctt aat acc aca ttc cca aga agt tac ttt aga tgc 644
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 Thr His Lys Pro Thr Gln Gly Cys Lys Ala Thr Lys Gln Val Gln Lys
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Ser Trp Asn Ala Ser Cys Gly Asp Asp Ser Ala Thr Pro Val Ser Cys
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Asn Gly Gly Asp Ser Gly Glu Ser Lys Lys Lys Arg Leu Gly Val Gly
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Lys Gly Lys Arg Gly Cys Tyr Thr Arg Lys Thr Arg Ser His Thr Arg
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Gly Gln Lys Glu Ile Leu Asn Thr Thr Phe Pro Arg Ser Tyr Phe Arg
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Cys Thr His Lys Pro Thr Gln Gly Cys Lys Ala Thr Lys Gln Val Gln
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Lys Gln Asp Gln Asp Ser Glu Met Phe Gln Ile Thr Tyr Ile Gly Tyr
195 200 205

His Thr Cys Thr Ala Asn Asp Gln Thr His Ala Lys Thr Glu Pro Phe
210 215 220

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Asp Gln Glu Ile Ile Met Asp Ser Glu Lys Thr Leu Ala Ala Ser Thr
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 Ala Gln Asn His Val Asn Ala Met Val Gln Glu Gln Glu Asn Asn Thr
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 Asn Asn Gly Asp Gln Ser Lys Asp Tyr Tyr Glu Gly Ser Ser Thr Gly
 275 280 285
 Glu Asp Leu Ser Leu Val Trp Gln Glu Thr Met Met Phe Asp Asp His
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 Gln Asn His Tyr Tyr Cys Gly Glu Thr Ser Thr Thr Ser His Gln Phe
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 Gly Val Thr Arg Met Arg Val Glu Glu Asp Pro Pro Thr Ser Ala Leu
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Ser Thr Pro Val Ala Ala Asn Arg Arg Ser Ser Leu Thr Val Pro Val	
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Thr Thr Val Asp Met Ile Glu Ser Lys Lys Val Thr Ser Pro Thr Ser	
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Arg Ile Asp Phe Pro Gln Val Gln Lys Leu Leu Val Glu Gln Met Ala	
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 50 55 60

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Ser Pro Pro Lys Lys Arg Lys Ser Pro Ala Arg Glu Asp Ala Phe Ser
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Cys Ala Val Ile Gly Gly Val Ser Glu Ser Ser Ser Thr Asp Gln Asp
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Glu Tyr Leu Cys Lys Lys Gln Arg Glu Glu Thr Val Val Lys Glu Lys
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 130 135 140

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10 15 20

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Ala Ser Ala Ser Lys Val Val Glu Lys Lys Trp Leu Val Lys Asp Glu
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Lys Arg Asn Met Leu Gln Asp Glu Ile Asn Arg Val Asn Ser Glu Asn
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aag aag cta acc gaa atg tta gca aga gtc tgt gag aag tac tat gct 246
Lys Lys Leu Thr Glu Met Leu Ala Arg Val Cys Glu Lys Tyr Tyr Ala
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ctt aat aat ctt atg gag gag ttg cag agt cga aag agt cct gaa agt 294
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 75 80 85

gtt aac ttt cag aac aaa cag cta acg ggg aaa cga aaa caa gaa ctt 342
 Val Asn Phe Gln Asn Lys Gln Leu Thr Gly Lys Arg Lys Lys Gln Glu Leu
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 Asp Glu Phe Val Ser Ser Pro Ile Gly Leu Ser Leu Gly Pro Ile Glu
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 155 160 165

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cga agt gca gaa gat cca tct ttc ttg gta gcc act tac gaa ggg aca 630
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cat aac cac acc gga cca cat gca agt gtg tcc agg aca gtg aaa ctt 678
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 205 210 215

gat cta gtt caa ggt ggg ctt gaa cca gtt gag gaa aag aaa gag aga 726
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Ile	Asn 50	Arg	Val	Asn	Ser	Glu 55	Asn	Lys	Lys	Leu	Thr 60	Glu	Met	Leu	Ala
Arg 65	Val	Cys	Glu	Lys	Tyr 70	Tyr	Ala	Leu	Asn	Asn 75	Leu	Met	Glu	Glu	Leu 80
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Asp	Asn	Pro	Ser	Pro 165	Arg	Ala	Tyr	Phe	Arg 170	Cys	Ser	Phe	Ser	Pro 175	Ser
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Pro 225	Val	Glu	Glu	Lys	Lys 230	Glu	Arg	Gly	Thr	Ile 235	Gln	Glu	Val	Leu	Val 240
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 Ala Gly Ile His Gly Val Glu Glu Phe Leu Lys Leu Ile Gly Gln Ser
 40 45 50 55

caa caa cca acg gag aag agt cag acg gag ata acc gcg gtg act gac 247
 Gln Gln Pro Thr Glu Lys Ser Gln Thr Glu Ile Thr Ala Val Thr Asp
 60 65 70

gtc gcc gtt aac agc ttc aag aag gtc att tct cta ctc ggt aga tct 295
 Val Ala Val Asn Ser Phe Lys Lys Val Ile Ser Leu Leu Gly Arg Ser
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 Arg Thr Gly His Ala Arg Phe Arg Arg Ala Pro Ala Ser Thr Gln Thr
 90 95 100

ccg ttt aag caa acg ccg gtg gtt gag gag gag gtg gag gtg gag gag 391
 Pro Phe Lys Gln Thr Pro Val Val Glu Glu Glu Val Glu Val Glu Glu
 105 110 115

aag aag cca gaa aca agc tcc gtg tta aca aaa cag aaa aca gag caa 439
 Lys Lys Pro Glu Thr Ser Ser Val Leu Thr Lys Gln Lys Thr Glu Gln
 120 125 130 135

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 140 145 150

cat cgt cgt cct cct cta tca cac aat aac aac aac aat cag aat caa 535
 His Arg Arg Pro Pro Leu Ser His Asn Asn Asn Asn Asn Gln Asn Gln
 155 160 165

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Asn	Ser	Phe	Met	Ser	Ser	His	Arg	Cys	Asp	Thr	Asp	Ser	Thr	His	Met		
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Cys	Pro	Ala	Arg	Lys	His	Val	Glu	Arg	Ala	Leu	Asp	Asp	Ala	Met	Met		
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Leu	Ile	Val	Thr	Tyr	Glu	Gly	Asp	His	Asn	His	Ala	Leu	Val	Leu	Glu		
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Val	Tyr	Cys	Pro	Thr	Pro	Ile	His	Arg	Arg	Pro	Pro	Leu	Ser	His	Asn	145	150	155	160
Asn	Asn	Asn	Asn	Gln	Asn	Gln	Thr	Lys	Asn	Gly	Ser	Ser	Ser	Ser	Ser	165	170	175	
Pro	Pro	Met	Leu	Ala	Asn	Gly	Ala	Pro	Ser	Thr	Ile	Asn	Phe	Ala	Pro	180	185	190	
Ser	Pro	Pro	Val	Ser	Ala	Thr	Asn	Ser	Phe	Met	Ser	Ser	His	Arg	Cys	195	200	205	
Asp	Thr	Asp	Ser	Thr	His	Met	Ser	Ser	Gly	Phe	Glu	Phe	Thr	Asn	Pro	210	215	220	
Ser	Gln	Leu	Ser	Gly	Ser	Arg	Gly	Lys	Pro	Pro	Leu	Ser	Ser	Ala	Ser	225	230	235	240
Leu	Lys	Arg	Arg	Cys	Asn	Ser	Ser	Pro	Ser	Ser	Arg	Cys	His	Cys	Ser	245	250	255	

636150: 636150

Lys Lys Arg Lys Ser Arg Val Lys Arg Val Ile Arg Val Pro Ala Val
260 265 270

Ser Ser Lys Met Ala Asp Ile Pro Ser Asp Glu Phe Ser Trp Arg Lys
275 280 285

Tyr Gly Gln Lys Pro Ile Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr
290 295 300

Lys Cys Ser Ser Val Arg Gly Cys Pro Ala Arg Lys His Val Glu Arg
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Ala Leu Asp Asp Ala Met Met Leu Ile Val Thr Tyr Glu Gly Asp His
325 330 335

Asn His Ala Leu Val Leu Glu Thr Thr Thr Met Asn His Asp Lys Thr
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Lys Ala Lys Lys Leu Lys Val Met Asn Gln Leu Val Glu Gly His Asp
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Leu Thr Thr Gln Leu Gln Gln Leu Leu Ser Gln Pro Gly Ser Gly Leu
25 30 35

gag gat cta gtg gct aaa atc tta gtg tgt ttc aat aac acc atc tcc 198
Glu Asp Leu Val Ala Lys Ile Leu Val Cys Phe Asn Asn Thr Ile Ser
40 45 50

gtt ctt gat acc ttc gaa ccc atc tcc tcc tcc tca tcc ctc gcc gcc 246
Val Leu Asp Thr Phe Glu Pro Ile Ser Ser Ser Ser Ser Leu Ala Ala
55 60 65

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Val Glu Gly Ser Gln Asn Ala Ser Cys Asp Asn Asp Gly Lys Phe Glu
70 75 80

gat tcc ggc gat agt cgg aaa aga ttg gga ccc gtt aag ggt aaa aga 342
Asp Ser Gly Asp Ser Arg Lys Arg Leu Gly Pro Val Lys Gly Lys Arg
85 90 95 100

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Gly Cys Tyr Lys Arg Lys Lys Arg Ser Glu Thr Cys Thr Ile Glu Ser
105 110 115

act ata ctt gag gac gca ttt tct tgg agg aaa tat gga caa aag gag 438
Thr Ile Leu Glu Asp Ala Phe Ser Trp Arg Lys Tyr Gly Gln Lys Glu
120 125 130

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Ile Leu Asn Ala Lys Phe Pro Arg Ser Tyr Phe Arg Cys Thr His Lys
135 140 145

tat acc caa ggg tgc aag gca aca aag caa gtc cag aag gtt gag ctc 534
Tyr Thr Gln Gly Cys Lys Ala Thr Lys Lys Gln Val Gln Lys Val Glu Leu
150 155 160

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Glu Pro Lys Met Phe Ser Ile Thr Tyr Ile Gly Asn His Thr Cys Asn
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Thr Asn Ala Glu Thr Pro Lys Ser Lys Thr Cys Asp His His Asp Glu
185 190 195

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Ile Phe Met Asp Ser Glu Asp His Lys Ser Pro Ser Leu Ser Thr Ser
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215 220 225

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Asn Asp Leu Ser Leu Val Trp Pro Glu Met Val Phe Glu Glu Asp Tyr
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His His Gln Ala Ser Tyr Val Asn Gly Lys Thr Ser Thr Ser Ile Asp
245 250 255 260

gtt ttg ggt tct cag gat ctc atg gtg ttt gga ggt ggc ggc gat ttc 870
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265 270 275

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Glu Phe Ser Glu Asn Glu His Phe Ser Ile Phe Ser Ser Cys Ser Asn
280 285 290

cta tct tgagtttacc actactatag gactaagacc atgagtttta atcattaatt 974
Leu Ser

aggccatgta gagtggaaaa catataatac atattttgcc cttttctcta atgagtgtat 1034

gtactgtaca tatagtacta taaataaaaac tcttgctgga ttaaaacaaa aaaaaaaaaa 1094

1099

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Gly Ser Gly Leu Glu Asp Leu Val Ala Lys Ile Leu Val Cys Phe Asn
35 40 45

Asn Thr Ile Ser Val Leu Asp Thr Phe Glu Pro Ile Ser Ser Ser Ser
50 55 60

Ser Leu Ala Ala Val Glu Gly Ser Gln Asn Ala Ser Cys Asp Asn Asp
65 70 75 80

Gly Lys Phe Glu Asp Ser Gly Asp Ser Arg Lys Arg Leu Gly Pro Val
85 90 95

Lys Gly Lys Arg Gly Cys Tyr Lys Arg Lys Lys Arg Ser Glu Thr Cys
100 105 110

Thr Ile Glu Ser Thr Ile Leu Glu Asp Ala Phe Ser Trp Arg Lys Tyr
115 120 125

Gly Gln Lys Glu Ile Leu Asn Ala Lys Phe Pro Arg Ser Tyr Phe Arg
130 135 140

Cys Thr His Lys Tyr Thr Gln Gly Cys Lys Ala Thr Lys Gln Val Gln
145 150 155 160

Lys Val Glu Leu Glu Pro Lys Met Phe Ser Ile Thr Tyr Ile Gly Asn
165 170 175

His Thr Cys Asn Thr Asn Ala Glu Thr Pro Lys Ser Lys Thr Cys Asp
180 185 190

His His Asp Glu Ile Phe Met Asp Ser Glu Asp His Lys Ser Pro Ser
195 200 205

Leu Ser Thr Ser Met Lys Glu Glu Asp Asn Pro His Arg His His Gly
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225 230 235 240

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Val Glu Ala Ala Asn Arg Ser Ala Ile Glu Ser Cys His Gly Val Leu																
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aat ctc ttg tca caa cga acc agt gat ccc aaa tcc tta acg gtt gaa																153
Asn Leu Leu Ser Gln Arg Thr Ser Asp Pro Lys Ser Leu Thr Val Glu																
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Thr Gly Glu Val Ser Lys Phe Lys Arg Val Ala Ser Leu Leu Thr																
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Arg Gly Leu Gly His Gly Lys Phe Arg Ser Thr Asn Lys Phe Arg Ser																
55 60 65																
tct ttt cct caa cac atc ttc tta gag agt cct att tgc tgc ggt aat																297
Ser Phe Pro Gln His Ile Phe Leu Glu Ser Pro Ile Cys Cys Gly Asn																
70 75 80																
gat cta agt ggt gat tac act caa gtt ctt gca cca gag cca ctt cag																345
Asp Leu Ser Gly Asp Tyr Thr Gln Val Leu Ala Pro Glu Pro Leu Gln																
85 90 95																
atg gtt cca gct tct gct gtt tat aat gaa atg gag cca aaa cac caa																393
Met Val Pro Ala Ser Ala Val Tyr Asn Glu Met Glu Pro Lys His Gln																
100 105 110 115																

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 Leu Gly His Pro Ser Leu Met Leu Ser His Lys Met Cys Val Asp Lys
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 Ser Phe Leu Glu Leu Lys Pro Pro Phe Arg Ala Pro Tyr Gln Leu
 135 140 145

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 Ile His Asn His Gln Gln Ile Ala Tyr Ser Arg Ser Asn Ser Gly Val
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 Asn Leu Lys Phe Asp Gly Ser Gly Ser Ser Cys Tyr Thr Pro Ser Val
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tca aac gga tca aga tca ttt gtg tca tct ctt agc atg gat gct agt 633
 Ser Asn Gly Ser Arg Ser Phe Val Ser Ser Leu Ser Met Asp Ala Ser
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 Val Thr Asp Tyr Asp Arg Asn Ser Phe His Leu Thr Gly Leu Ser Arg
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 Gly Ser Asp Gln Gln His Thr Arg Lys Met Cys Ser Gly Ser Leu Lys
 215 220 225

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 Cys Gly Ser Arg Ser Lys Cys His Cys Ser Lys Lys Arg Lys Leu Arg
 230 235 240

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 Val Lys Arg Ser Ile Lys Val Pro Ala Ile Ser Asn Lys Ile Ala Asp
 245 250 255

att cct cca gat gag tat tct tgg agg aag tat gga cag aaa ccg ata 873
 Ile Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly Gln Lys Pro Ile
 260 265 270 275

aag ggt tca ccg cat cca cgg gga tac tat aaa tgc agc agt gtg aga 921
 Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser Ser Val Arg
 280 285 290

ggt tgt cca gca agg aag cat gtg gag cga tgt att gat gaa act tca 969
 Gly Cys Pro Ala Arg Lys His Val Glu Arg Cys Ile Asp Glu Thr Ser
 295 300 305

atg tta att gta act tac gaa ggc gag cat aac cat tca aga ata ttg 1017
 Met Leu Ile Val Thr Tyr Glu Gly Glu His Asn His Ser Arg Ile Leu
 310 315 320

tct tca caa tca gct cac act tgatgataca gagtcaatat gtatgtcctt 1068
 Ser Ser Gln Ser Ala His Thr
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35 40 45

Leu Leu Thr Arg Gly Leu Gly His Gly Lys Phe Arg Ser Thr Asn Lys
50 55 60

Phe Arg Ser Ser Phe Pro Gln His Ile Phe Leu Glu Ser Pro Ile Cys
65 70 75 80

Cys Gly Asn Asp Leu Ser Gly Asp Tyr Thr Gln Val Leu Ala Pro Glu
85 90 95

Pro Leu Gln Met Val Pro Ala Ser Ala Val Tyr Asn Glu Met Glu Pro
100 105 110

Lys His Gln Leu Gly His Pro Ser Leu Met Leu Ser His Lys Met Cys
115 120 125

Val Asp Lys Ser Phe Leu Glu Leu Lys Pro Pro Pro Phe Arg Ala Pro
130 135 140

Tyr Gln Leu Ile His Asn His Gln Gln Ile Ala Tyr Ser Arg Ser Asn
145 150 155 160

Ser Gly Val Asn Leu Lys Phe Asp Gly Ser Gly Ser Ser Cys Tyr Thr
165 170 175

Pro Ser Val Ser Asn Gly Ser Arg Ser Phe Val Ser Ser Leu Ser Met
180 185 190

Asp Ala Ser Val Thr Asp Tyr Asp Arg Asn Ser Phe His Leu Thr Gly
195 200 205

Leu Ser Arg Gly Ser Asp Gln Gln His Thr Arg Lys Met Cys Ser Gly
210 215 220

Ser Leu Lys Cys Gly Ser Arg Ser Lys Cys His Cys Ser Lys Lys Arg
 225 230 235 240

Lys Leu Arg Val Lys Arg Ser Ile Lys Val Pro Ala Ile Ser Asn Lys
 245 250 255

Ile Ala Asp Ile Pro Pro Asp Glu Tyr Ser Trp Arg Lys Tyr Gly Gln
 260 265 270

Lys Pro Ile Lys Gly Ser Pro His Pro Arg Gly Tyr Tyr Lys Cys Ser
 275 280 285

Ser Val Arg Gly Cys Pro Ala Arg Lys His Val Glu Arg Cys Ile Asp
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 Met Ala Met Gly Lys Tyr Ser Arg Val Asp
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 Ala Pro Thr Glu Ser Ile Asp Phe Ser Ala Asn Glu Arg Thr Lys Asp
 45 50 55

gta gat act act aag agt gat ttc aaa agt gaa gag gtt gat cga ggt 364
 Val Asp Thr Thr Lys Ser Asp Phe Lys Ser Glu Glu Val Asp Arg Gly
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Glu Thr Asn Glu Glu Lys Thr Asp Pro Glu Lys Ser Gly Glu Glu Asn	
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Ser Gly Glu Lys Thr Glu Ser Ala Glu Glu Arg Lys Glu Phe Asp Asp	
110 115 120	
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Lys Asn Gly Asp Gly Asp Arg Lys Asn Gly Asp Gly Glu Lys Asp Thr	
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Glu Ser Glu Ser Asp Glu Thr Lys Gln Lys Glu Lys Thr Gln Leu Glu	
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Glu Ser Ser Glu Glu Asn Lys Ser Glu Asp Ser Asn Gly Thr Glu Glu	
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Ala Gly Glu Thr Glu Glu Ser Thr Glu Lys Ser Lys Asp Val Phe Pro	
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Arg Cys Leu Val Ser Leu Pro Glu Gly Tyr Lys Arg Ser Ile Lys Trp	
285 290 295	

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Pro Ala Met Ser Asn Val Met Gly Thr Lys Arg Leu Pro Phe Pro Gly	
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430 435 440	
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Glu Asp Val Gly Ile Trp Lys Ala Met Ser Lys Leu Thr Lys Ala Met	
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Cys Trp Glu Leu Met Thr Ile Lys Lys Asp Glu Leu Asn Glu Val Gly	
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cct Pro	gca Ala	caa Gln	gag Glu 590	gat Asp	ttc Phe	aca Thr	gca Ala	gac Asp 595	cat His	gaa Glu	cgc Arg	tgg Trp	aag Lys 600	act Thr	att Ile	1948
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 765 770

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Asp Phe Lys Ser Glu Glu Val Asp Arg Gly Ser Lys Ser Phe Pro Asp
 65 70 75 80

Glu Lys Asn Glu Glu Thr Glu Val Val Thr Glu Thr Asn Glu Glu Lys
 85 90 95

Thr Asp Pro Glu Lys Ser Gly Glu Glu Asn Ser Gly Glu Lys Thr Glu
 100 105 110

Ser Ala Glu Glu Arg Lys Glu Phe Asp Asp Lys Asn Gly Asp Gly Asp
 115 120 125

Arg Lys Asn Gly Asp Gly Glu Lys Asp Thr Glu Ser Glu Ser Asp Glu
 130 135 140

Thr Lys Gln Lys Glu Lys Thr Gln Leu Glu Glu Ser Ser Glu Glu Asn
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Lys Ser Glu Asp Ser Asn Gly Thr Glu Glu Asn Ala Gly Glu Ser Glu
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 180 185 190

Ser Thr Glu Lys Ser Lys Asp Val Phe Pro Ala Gly Asp Gln Ala Glu
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 Ile Thr Lys Glu Ser Ser Thr Gly Ser Gly Ala Trp Ser Thr Gln Leu
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 Val Glu Ser Gln Asn Glu Lys Lys Ala Gln Val Ser Ser Ile Lys Trp
 225 230 235 240
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ctc Leu	gga Gly 555	att Ile	gag Glu	ggc Gly	ttt Phe	gct Ala	gaa Glu 560	ttg Leu	cct Pro	aag Lys	cac His	tgt Cys 565	ttg Leu	gct Ala	ctt Leu	1793
tgt Cys	tac Tyr 570	ggg Gly	ttt Phe	ttc Phe	ata Ile	gca Ala 575	gct Ala	ttg Leu	att Ile	gtg Val	aat Asn 580	ctc Leu	tta Leu	aga Arg	gat Asp	1841
att Ile 585	aca Thr	ccg Pro	cct Pro	aag Lys	atc Ile 590	tct Ser	cag Gln	ttc Phe	atc Ile	ccg Pro 595	atc Ile	cca Pro	atg Met	gca Ala	atg Met 600	1889

gct gtc cca ttc tac att gga gct tac ttc gcc att gac atg ttt gtt 1937
Ala Val Pro Phe Tyr Ile Gly Ala Tyr Phe Ala Ile Asp Met Phe Val
605 610 615

ggg act gtg ata ttg ttc gta tgg gaa cgg atc aac agg aaa gat gca 1985
Gly Thr Val Ile Leu Phe Val Trp Glu Arg Ile Asn Arg Lys Asp Ala
620 625 630

gag gac ttt gca ggt gca gta gca tca gga ctg atc tgt ggt gat ggg 2033
Glu Asp Phe Ala Gly Ala Val Ala Ser Gly Leu Ile Cys Gly Asp Gly
635 640 645

atc tgg act ata cca tcc gca atc ctt tca atc tta agg atc aac cct 2081
Ile Trp Thr Ile Pro Ser Ala Ile Leu Ser Ile Leu Arg Ile Asn Pro
650 655 660

ccc att tgt atg tac ttt gga ccg tcc tca gca aga tagagatgcc 2127
Pro Ile Cys Met Tyr Phe Gly Pro Ser Ser Ala Arg
665 670 675

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cttgtggccg tcagaatcga aacagttgtc ttcatatgtt gtgtagatat gtttagtatc 2247

tcagctcgca agaacaaaat gttgttgcaa atctcttcaa atgttttagt caatgttggt 2307

gtatgtcccc gggatgttgt ctccttgaat gctttcattc acaagctcaa agagttttac 2367

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35 40 45

Leu Gly Thr Leu Phe Cys Ile Ile Thr His Lys Leu Asn Leu Thr Val
50 55 60

Gly Ile Ile Pro Ser Leu Asn Val Ala Ala Gly Leu Leu Gly Phe Phe
65 70 75 80

Phe Val Lys Ser Trp Thr Gly Phe Leu Ser Lys Leu Gly Phe Thr Val
 85 90 95
 Lys Pro Phe Thr Lys Gln Glu Asn Thr Val Ile Gln Thr Cys Val Val
 100 105 110
 Ala Cys Tyr Gly Leu Ala Phe Ser Gly Gly Phe Gly Ser Tyr Leu Ile
 115 120 125
 Ala Met Asp Glu Lys Thr Tyr Lys Leu Ile Gly Ala Asp Tyr Pro Gly
 130 135 140
 Asn His Ala Glu Asp Val Ile Asn Pro Gly Leu Trp Trp Met Ile Gly
 145 150 155 160
 Phe Leu Phe Val Val Ser Phe Leu Gly Leu Phe Ser Leu Val Pro Leu
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 Arg Lys Val Met Val Leu Asp Tyr Lys Leu Thr Tyr Pro Ser Gly Thr
 180 185 190
 Ala Thr Ala Met Leu Ile Asn Ser Phe His Thr Asn Thr Gly Ala Glu
 195 200 205
 Leu Ala Gly Asn Gln Val Lys Cys Leu Gly Lys Tyr Leu Ser Leu Ser
 210 215 220
 Leu Ile Trp Ser Cys Phe Lys Trp Phe Phe Ser Gly Ile Gly Asp Ala
 225 230 235 240
 Cys Gly Phe Asp Asn Phe Pro Thr Leu Gly Leu Thr Leu Phe Lys Asn
 245 250 255
 Thr Phe Tyr Phe Asp Phe Ser Pro Thr Tyr Ile Gly Cys Gly Leu Ile
 260 265 270
 Cys Pro His Ile Val Asn Cys Ser Val Leu Leu Gly Ala Ile Ile Ser
 275 280 285
 Trp Gly Ile Leu Trp Pro Phe Val Ser Gln His Ala Gly Asp Trp Tyr
 290 295 300
 Pro Ala Asp Leu Gly Ser Asn Asp Phe Lys Gly Leu Tyr Gly Tyr Lys
 305 310 315 320
 Val Phe Ile Ala Ile Ala Ile Ile Leu Gly Asp Gly Leu Tyr Asn Leu
 325 330 335
 Val Lys Ile Ile Ala Val Thr Val Lys Glu Leu Cys Ser Ser Arg Ser
 340 345 350
 Arg Arg Leu Asn Leu Pro Ile Val Thr Asp Gly Val Asp Asp Ser Glu
 355 360 365
 Ala Ser Glu Ile Leu Leu Val Lys Lys Lys Arg Asp Glu Val Phe Leu
 370 375 380

Lys Asp Arg Ile Pro Leu Glu Phe Ala Ile Ala Gly Tyr Val Gly Leu
 385 390 395 400
 Ala Ala Ile Ser Thr Ala Thr Ile Pro Ile Ile Phe Pro Pro Leu Lys
 405 410 415
 Trp Tyr Phe Val Leu Cys Ser Tyr Phe Ile Ala Pro Ala Leu Ala Phe
 420 425 430
 Cys Asn Ser Tyr Gly Thr Gly Leu Thr Asp Trp Ser Leu Ala Ser Thr
 435 440 445
 Tyr Gly Lys Ile Gly Leu Phe Ile Ile Ala Ser Val Val Gly Ser Asp
 450 455 460
 Gly Gly Val Ile Ala Gly Leu Ala Ala Cys Gly Val Met Met Ser Ile
 465 470 475 480
 Val Ser Thr Ala Ala Asp Leu Met Gln Asp Phe Lys Thr Gly Tyr Leu
 485 490 495
 Thr Leu Ser Ser Ala Lys Ser Met Phe Val Ser Gln Leu Val Gly Thr
 500 505 510
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 515 520 525
 Ala Phe Asp Ile Gly Asp Pro Asn Gly Pro Tyr Lys Ala Pro Tyr Ala
 530 535 540
 Val Ile Phe Arg Glu Met Ala Ile Leu Gly Ile Glu Gly Phe Ala Glu
 545 550 555 560
 Leu Pro Lys His Cys Leu Ala Leu Cys Tyr Gly Phe Phe Ile Ala Ala
 565 570 575
 Leu Ile Val Asn Leu Leu Arg Asp Ile Thr Pro Pro Lys Ile Ser Gln
 580 585 590
 Phe Ile Pro Ile Pro Met Ala Met Ala Val Pro Phe Tyr Ile Gly Ala
 595 600 605
 Tyr Phe Ala Ile Asp Met Phe Val Gly Thr Val Ile Leu Phe Val Trp
 610 615 620
 Glu Arg Ile Asn Arg Lys Asp Ala Glu Asp Phe Ala Gly Ala Val Ala
 625 630 635 640
 Ser Gly Leu Ile Cys Gly Asp Gly Ile Trp Thr Ile Pro Ser Ala Ile
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 Met Asn Arg Glu Lys Leu
 1 5

atg aag atg gct aac act gtc cgc act ggc gga aag ggg aca gta aga 161
 Met Lys Met Ala Asn Thr Val Arg Thr Gly Gly Lys Gly Thr Val Arg
 10 15 20

aga aag aag aag gct gtt cac aag acc act aca acc gat gac aag agg 209
 Arg Lys Lys Lys Ala Val His Lys Thr Thr Thr Thr Asp Asp Lys Arg
 25 30 35

ctc cag agc act ctt aag aga gtt gga gtc aat tcc att ccc gcc att 257
 Leu Gln Ser Thr Leu Lys Arg Val Gly Val Asn Ser Ile Pro Ala Ile
 40 45 50

gaa gaa gtt aac att ttt aag gat gat gta gtc att cag ttc att aac 305
 Glu Glu Val Asn Ile Phe Lys Asp Asp Val Val Ile Gln Phe Ile Asn
 55 60 65 70

cct aaa gtt caa gct tca att gct gct aac aca tgg gtt gtg agt ggt 353
 Pro Lys Val Gln Ala Ser Ile Ala Ala Asn Thr Trp Val Val Ser Gly
 75 80 85

aca cca cag acg aaa aaa ttg caa gac att ctt cct cag att atc agc 401
 Thr Pro Gln Thr Lys Lys Leu Gln Asp Ile Leu Pro Gln Ile Ile Ser
 90 95 100

caa ctt gga cca gat aac ttg gac aac ctg aag aag cta gca gag caa 449
 Gln Leu Gly Pro Asp Asn Leu Asp Asn Leu Lys Lys Leu Ala Glu Gln
 105 110 115

ttc cag aaa caa gct cca ggt gca ggt gat gtc cca gca aca atc caa 497
 Phe Gln Lys Gln Ala Pro Gly Ala Gly Asp Val Pro Ala Thr Ile Gln
 120 125 130

gaa gag gac gat gat gat gat gtc cca gat ctt gta gtg gga gag act 545
 Glu Glu Asp Asp Asp Asp Val Pro Asp Leu Val Val Gly Glu Thr
 135 140 145 150

ttc gag acc cct gct act gaa gag gct ccc aaa gct gct gct tct 590
 Phe Glu Thr Pro Ala Thr Glu Glu Ala Pro Lys Ala Ala Ala Ser
 155 160 165

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gtcgctcgac ctcttctgag cactgtcaga ttcttgTTTT ctctaagtct tgcgaacaga 710
 aagacttggt tttattatca cttgatgctt tttggTccga acagcaattt tccttttatt 770
 aaggTtagat cgctttttgt ttaccacctg ttcaaTgag tactactatg tcctgtcgct 830
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 Thr Thr Asp Asp Lys Arg Leu Gln Ser Thr Leu Lys Arg Val Gly Val
 35 40 45
 Asn Ser Ile Pro Ala Ile Glu Glu Val Asn Ile Phe Lys Asp Asp Val
 50 55 60
 Val Ile Gln Phe Ile Asn Pro Lys Val Gln Ala Ser Ile Ala Ala Asn
 65 70 75 80
 Thr Trp Val Val Ser Gly Thr Pro Gln Thr Lys Lys Leu Gln Asp Ile
 85 90 95
 Leu Pro Gln Ile Ile Ser Gln Leu Gly Pro Asp Asn Leu Asp Asn Leu
 100 105 110
 Lys Lys Leu Ala Glu Gln Phe Gln Lys Gln Ala Pro Gly Ala Gly Asp
 115 120 125
 Val Pro Ala Thr Ile Gln Glu Glu Asp Asp Asp Asp Asp Val Pro Asp
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 Lys Ala Ala Ala Ser
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<210> 103
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acc gga tca gct taggttttta cataactcgga gccctgacag agttgattct 639
Thr Gly Ser Ala
180

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679

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 35 40 45
 Gln Arg Tyr Leu Pro Ser Asn Glu Pro Asp Pro Glu Ser Tyr Pro Asp
 50 55 60
 Leu Leu Gly Pro Asp Ser Pro Ile Asp Ala Tyr Ser Cys Asp His Phe
 65 70 75 80
 Arg Met Tyr Asp Phe Lys Val Arg Arg Cys Ala Arg Gly Arg Ser His
 85 90 95
 Asp Trp Thr Glu Cys Pro Tyr Ala His Pro Gly Glu Lys Ala Arg Arg
 100 105 110
 Arg Asp Pro Arg Lys Tyr His Tyr Ser Gly Thr Ala Cys Pro Asp Phe
 115 120 125
 Arg Lys Gly Gly Cys Lys Lys Gly Asp Ser Cys Glu Phe Ala His Gly
 130 135 140
 Val Phe Glu Cys Trp Leu His Pro Ala Arg Tyr Arg Thr Gln Pro Cys
 145 150 155 160
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 Thr Gly Ser Ala
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 <223> G751

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Val Thr Asn Thr Cys Leu Lys Gln Gln Ser Asn Pro Pro Ser Pro Ala	
5 10 15 20	
act cct gtg gaa agg aag gca aga ccg gag aaa gac cag gct ttg aac	152
Thr Pro Val Glu Arg Lys Ala Arg Pro Glu Lys Asp Gln Ala Leu Asn	
25 30 35	
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Cys Pro Arg Cys Asn Ser Leu Asn Thr Lys Phe Cys Tyr Tyr Asn Asn	
40 45 50	
tac agc ctg acg cag ccc agg tac ttt tgt aaa gac tgc agg agg tat	248
Tyr Ser Leu Thr Gln Pro Arg Tyr Phe Cys Lys Asp Cys Arg Arg Tyr	
55 60 65	
tgg acc gca ggt ggt tcc ctc agg aac atc ccc gtc ggt ggc ggc gtc	296
Trp Thr Ala Gly Gly Ser Leu Arg Asn Ile Pro Val Gly Gly Gly Val	
70 75 80	
cgc aag aac aag aga tct tct tcc aat tcc tct tcc tct tca ccc tct	344
Arg Lys Asn Lys Arg Ser Ser Ser Asn Ser Ser Ser Ser Ser Pro Ser	
85 90 95 100	
tcg tct tct tct tca aag aaa cct ctt ttt gcc aac aac aac acg cct	392
Ser Ser Ser Ser Ser Lys Lys Pro Leu Phe Ala Asn Asn Asn Thr Pro	
105 110 115	
acg cct cct ctt cct cat ctt aac cct aag att ggt gaa gca gcc gct	440
Thr Pro Pro Leu Pro His Leu Asn Pro Lys Ile Gly Glu Ala Ala Ala	
120 125 130	
act aaa gtt caa gac ttg acg ttt tct caa ggg ttt ggg aac gcc cac	488
Thr Lys Val Gln Asp Leu Thr Phe Ser Gln Gly Phe Gly Asn Ala His	
135 140 145	
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Glu Val Lys Asp Leu Asn Leu Ala Phe Ser Gln Gly Phe Gly Ile Gly	
150 155 160	
cac aat cat cac agt agt atc cca gag ttt ctg caa gta gta ccc agc	584
His Asn His His Ser Ser Ile Pro Glu Phe Leu Gln Val Val Pro Ser	
165 170 175 180	
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Ser Ser Met Lys Asn Asn Pro Leu Val Ser Thr Ser Ser Ser Leu Glu	
185 190 195	
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Leu Leu Gly Ile Ser Ser Ser Ser Ala Ser Ser Asn Ser Arg Pro Ala	
200 205 210	

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 Phe Met Ser Tyr Pro Asn Val His Asp Ser Ser Val Tyr Thr Ala Ser
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 Gly Phe Gly Leu Ser Tyr Pro Gln Phe Gln Glu Phe Met Arg Pro Ala
 230 235 240
 ttg gga ttc tct ctt gat ggt ggg gat cct cta cgt caa gaa gag ggg 824
 Leu Gly Phe Ser Leu Asp Gly Gly Asp Pro Leu Arg Gln Glu Glu Gly
 245 250 255 260
 tcc agt ggc act aat aat gga agg ccg ttg ctg cca ttt gag agc ctc 872
 Ser Ser Gly Thr Asn Asn Gly Arg Pro Leu Leu Pro Phe Glu Ser Leu
 265 270 275
 ctc aaa ctt cca gtt tca tca tca agc acc aat agt ggt ggg aat ggc 920
 Leu Lys Leu Pro Val Ser Ser Ser Ser Thr Asn Ser Gly Gly Asn Gly
 280 285 290
 aat ctg aaa gag aat aat gat gag cat agt gat cat gaa cat gag aaa 968
 Asn Leu Lys Glu Asn Asn Asp Glu His Ser Asp His Glu His Glu Lys
 295 300 305
 gaa gaa gga gaa gct gac caa tct gtt ggg ttt tgg agt ggc atg tta 1016
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 325 330 335
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 35 40 45
 Tyr Tyr Asn Asn Tyr Ser Leu Thr Gln Pro Arg Tyr Phe Cys Lys Asp
 50 55 60
 Cys Arg Arg Tyr Trp Thr Ala Gly Gly Ser Leu Arg Asn Ile Pro Val
 65 70 75 80
 Gly Gly Gly Val Arg Lys Asn Lys Arg Ser Ser Ser Asn Ser Ser Ser
 85 90 95
 Ser Ser Pro Ser Ser Ser Ser Ser Ser Lys Lys Pro Leu Phe Ala Asn
 100 105 110
 Asn Asn Thr Pro Thr Pro Pro Leu Pro His Leu Asn Pro Lys Ile Gly
 115 120 125
 Glu Ala Ala Ala Thr Lys Val Gln Asp Leu Thr Phe Ser Gln Gly Phe
 130 135 140
 Gly Asn Ala His Glu Val Lys Asp Leu Asn Leu Ala Phe Ser Gln Gly
 145 150 155 160
 Phe Gly Ile Gly His Asn His His Ser Ser Ile Pro Glu Phe Leu Gln
 165 170 175
 Val Val Pro Ser Ser Ser Met Lys Asn Asn Pro Leu Val Ser Thr Ser
 180 185 190
 Ser Ser Leu Glu Leu Leu Gly Ile Ser Ser Ser Ser Ala Ser Ser Asn
 195 200 205
 Ser Arg Pro Ala Phe Met Ser Tyr Pro Asn Val His Asp Ser Ser Val
 210 215 220
 Tyr Thr Ala Ser Gly Phe Gly Leu Ser Tyr Pro Gln Phe Gln Glu Phe
 225 230 235 240
 Met Arg Pro Ala Leu Gly Phe Ser Leu Asp Gly Gly Asp Pro Leu Arg
 245 250 255
 Gln Glu Glu Gly Ser Ser Gly Thr Asn Asn Gly Arg Pro Leu Leu Pro
 260 265 270
 Phe Glu Ser Leu Leu Lys Leu Pro Val Ser Ser Ser Ser Thr Asn Ser
 275 280 285
 Gly Gly Asn Gly Asn Leu Lys Glu Asn Asn Asp Glu His Ser Asp His
 290 295 300
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Asp Ser Cys Lys Ser Thr Ala Ala Thr Leu Phe Cys Arg Ala Asp Ala																	
10 15 20																	
gcg ttt ctc tgc ggc gac tgc gac ggt aag atc cac aca gct aac aaa																	150
Ala Phe Leu Cys Gly Asp Cys Asp Gly Lys Ile His Thr Ala Asn Lys																	
25 30 35 40																	
ctc gca tca cgt cac gaa cga gtt tgg cta tgt gaa gta tgc gaa caa																	198
Leu Ala Ser Arg His Glu Arg Val Trp Leu Cys Glu Val Cys Glu Gln																	
45 50 55																	
gca cca gca cac gtc acg tgc aaa gct gac gcc gct gcg tta tgc gtc																	246
Ala Pro Ala His Val Thr Cys Lys Ala Asp Ala Ala Ala Leu Cys Val																	
60 65 70																	
acg tgc gac cgt gat atc cac tca gct aat cca ctc tct cgc cgc cac																	294
Thr Cys Asp Arg Asp Ile His Ser Ala Asn Pro Leu Ser Arg Arg His																	
75 80 85																	
gag cgc gta cca atc act cct ttc tac gac gct gta ggt cca gca aaa																	342
Glu Arg Val Pro Ile Thr Pro Phe Tyr Asp Ala Val Gly Pro Ala Lys																	
90 95 100																	
tcc gct tcc tcc tcc gtc aat ttc gta gat gaa gat ggc ggt gac gtc																	390
Ser Ala Ser Ser Ser Val Asn Phe Val Asp Glu Asp Gly Gly Asp Val																	
105 110 115 120																	
act gct tcg tgg ctt tta gct aaa gaa gga atc gaa atc act aat ttg																	438
Thr Ala Ser Trp Leu Leu Ala Lys Glu Gly Ile Glu Ile Thr Asn Leu																	
125 130 135																	
ttc tcc gat ctt gat tat ccg aag att gag gta acg tcg gag gag aat																	486
Phe Ser Asp Leu Asp Tyr Pro Lys Ile Glu Val Thr Ser Glu Glu Asn																	
140 145 150																	
agc tcc ggt aac gac gga gtt gtt cct gtg cag aat aag ttg ttt ctt																	534
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              20              25              30

Gly  Lys  Ile  His  Thr  Ala  Asn  Lys  Leu  Ala  Ser  Arg  His  Glu  Arg  Val
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<223> G902

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aagacttata agattgaaaa agcaag atg cgg att ttg tgc gat gct tgc gag 173
 Met Arg Ile Leu Cys Asp Ala Cys Glu
 1 5

aac gca gcc gca atc atc ttt tgc gcc gcc gat gaa gct gcc ctt tgt 221
 Asn Ala Ala Ala Ile Ile Phe Cys Ala Ala Asp Glu Ala Ala Leu Cys
 10 15 20 25

cgc ccc tgc gat gaa aaa gtt cat atg tgc aac aag cta gct agt cgg 269
 Arg Pro Cys Asp Glu Lys Val His Met Cys Asn Lys Leu Ala Ser Arg
 30 35 40

cat gta cgt gtt ggt tta gct gaa cca agc aat gcc cca tgc tgt gat 317
 His Val Arg Val Gly Leu Ala Glu Pro Ser Asn Ala Pro Cys Cys Asp
 45 50 55

ata tgc gaa aat gca cct gcc ttc ttt tac tgt gag ata gac ggt agt 365
 Ile Cys Glu Asn Ala Pro Ala Phe Phe Tyr Cys Glu Ile Asp Gly Ser
 60 65 70

tct ctt tgt ctg caa tgt gac atg gta gta cat gtt ggt ggc aag aga 413
 Ser Leu Cys Leu Gln Cys Asp Met Val Val His Val Gly Gly Lys Arg
 75 80 85

aca cac ggt cgg ttt ctt ttg ctg aga cag aga atc gag ttt cca ggg 461
 Thr His Gly Arg Phe Leu Leu Arg Gln Arg Ile Glu Phe Pro Gly
 90 95 100 105

gat aag cct aaa gaa aac aat acg agg gac aat ttg cag aac caa aga 509
 Asp Lys Pro Lys Glu Asn Asn Thr Arg Asp Asn Leu Gln Asn Gln Arg
 110 115 120

gtc tct aca aat gga aat ggt gaa gcc aat ggg aag att gat gac gaa 557
 Val Ser Thr Asn Gly Asn Gly Glu Ala Asn Gly Lys Ile Asp Asp Glu
 125 130 135

atg att gat cta aat gct aat cca caa aga gta cat gag cca tca tca 605
 Met Ile Asp Leu Asn Ala Asn Pro Gln Arg Val His Glu Pro Ser Ser
 140 145 150

aat aac aac ggg att gat gta aat aac gag aac aat cac gag cct gca 653
 Asn Asn Asn Gly Ile Asp Val Asn Asn Glu Asn Asn His Glu Pro Ala
 155 160 165

ggc ctt gta cca gtt gga ccc ttt aaa cga gag tct gag aag 695
 Gly Leu Val Pro Val Gly Pro Phe Lys Arg Glu Ser Glu Lys
 170 175 180

tgataaggtg agagagagag agagaaagag actctttact ctgattcaaa aaatcagttt 755

aagaagaaga ttgtaaaaag tttcaagaac tggagatttc atgtccgttt tttttccttc 815

600
500
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886

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<212> PRT

<213> Arabidopsis thaliana

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<223> G902

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20 25 30

His Met Cys Asn Lys Leu Ala Ser Arg His Val Arg Val Gly Leu Ala
35 40 45

Glu Pro Ser Asn Ala Pro Cys Cys Asp Ile Cys Glu Asn Ala Pro Ala
50 55 60

Phe Phe Tyr Cys Glu Ile Asp Gly Ser Ser Leu Cys Leu Gln Cys Asp
65 70 75 80

Met Val Val His Val Gly Gly Lys Arg Thr His Gly Arg Phe Leu Leu
85 90 95

Leu Arg Gln Arg Ile Glu Phe Pro Gly Asp Lys Pro Lys Glu Asn Asn
100 105 110

Thr Arg Asp Asn Leu Gln Asn Gln Arg Val Ser Thr Asn Gly Asn Gly
115 120 125

Glu Ala Asn Gly Lys Ile Asp Asp Glu Met Ile Asp Leu Asn Ala Asn
130 135 140

Pro Gln Arg Val His Glu Pro Ser Ser Asn Asn Asn Gly Ile Asp Val
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caaccatcg atg gtg gtc atg tca cga gta agc ttc tac tct tct ttc ttg 171

Met Val Val Met Ser Arg Val Ser Phe Tyr Ser Ser Phe Leu

1

5

10

cta cta ctg tta gag gtc gtt gtc gct agc agc gag ttt gat gat gaa 219

Leu Leu Leu Leu Glu Val Val Val Ala Ser Ser Glu Phe Asp Asp Glu

15

20

25

30

gga aga aca tcg ttc agt cca acc acg gct ata atc atg atc gta ctc 267

Gly Arg Thr Ser Phe Ser Pro Thr Thr Ala Ile Ile Met Ile Val Leu

35

40

45

gtt agt gtt ttc ttc gca ctt gga tgt atc tcc gtc tac atg agg agg 315

Val Ser Val Phe Phe Ala Leu Gly Cys Ile Ser Val Tyr Met Arg Arg

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55

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Cys Leu Gln His Ala Leu Gly Met Asp Ser Gly Gly Gly Pro Gly Asn

65

70

75

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Trp Leu Asn Val Arg Gln Thr Thr Glu Pro Gly Leu Asp Ala Ser Val

80

85

90

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Ile Glu Thr Phe Pro Thr Phe Pro Tyr Ser Thr Val Lys Thr Leu Arg

95

100

105

110

atc ggt aaa gaa gct ttg gag tgt ccc gtt tgt ctc aac gag ttc gag 507

Ile Gly Lys Glu Ala Leu Glu Cys Pro Val Cys Leu Asn Glu Phe Glu

115

120

125

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Pro Gly Cys Ile Asp Ala Trp Leu Arg Ser Gln Thr Thr Cys Pro Leu

145

150

155

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Cys Arg Ala Asn Leu Val Pro Val Pro Gly Glu Ser Val Ser Ser Glu

160

165

170

ata ccc ggt tta gct aga gaa acc ggt cag aac tct ctc aga acg ccg 699

Ile Pro Gly Leu Ala Arg Glu Thr Gly Gln Asn Ser Leu Arg Thr Pro

175

180

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190

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G905 (130)..(1272)

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 Ile Asp Ser Val Ala Trp Thr Gly Asn Gln Ser Met Pro Arg Lys Ser
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 Met Ser Thr Gly Trp Lys Leu Ala Glu Leu Tyr Ser Pro Ala Ser Ser
 225 230 235
 ccg ggc caa ccg gag gag aat ctc gac cgg tat acg ctg agg tta cca 891
 Pro Gly Gln Pro Glu Glu Asn Leu Asp Arg Tyr Thr Leu Arg Leu Pro
 240 245 250
 caa gag ata cat gac cag ctt gtg aac tcc agc ctg gga aag caa ggg 939
 Gln Glu Ile His Asp Gln Leu Val Asn Ser Ser Leu Gly Lys Gln Gly
 255 260 265 270
 tca aaa ggc caa ctg gcc tta cct caa gaa agg agc tcg gtt aga ggg 987
 Ser Lys Gly Gln Leu Ala Leu Pro Gln Glu Arg Ser Ser Val Arg Gly
 275 280 285
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 305 310 315
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 Pro Pro Tyr His Thr Arg Ser Ile Gln Ser Pro Asp Glu Ile Ile Asn
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Val Phe Phe Ala Leu Gly Cys Ile Ser Val Tyr Met Arg Arg Cys Leu
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Gln His Ala Leu Gly Met Asp Ser Gly Gly Gly Pro Gly Asn Trp Leu
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Lys Glu Ala Leu Glu Cys Pro Val Cys Leu Asn Glu Phe Glu Asp Asp
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Glu Thr Leu Arg Leu Ile Pro Gln Cys Cys His Val Phe His Pro Gly
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Cys Ile Asp Ala Trp Leu Arg Ser Gln Thr Thr Cys Pro Leu Cys Arg
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Ala Asn Leu Val Pro Val Pro Gly Glu Ser Val Ser Ser Glu Ile Pro
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Gly Leu Ala Arg Glu Thr Gly Gln Asn Ser Leu Arg Thr Pro Ile Asp
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Asp Asn Arg Lys Arg Val Leu Thr Ser Pro Asp Glu Arg Leu Ile Asp
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Ser Val Ala Trp Thr Gly Asn Gln Ser Met Pro Arg Lys Ser Met Ser
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Gln Pro Glu Glu Asn Leu Asp Arg Tyr Thr Leu Arg Leu Pro Gln Glu
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gag gca cta ttt gaa gct aga caa gct gct ata gct caa gag aag gtt 195																
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aaa gct gtt gaa gca ccg atg ctt tat agt tgt gga atc tgt aac aaa 243																
Lys	Ala	Val	Glu	Ala	Pro	Met	Leu	Tyr	Ser	Cys	Gly	Ile	Cys	Asn	Lys	
			60			65					70				75	
ggt tac agg agt tcc aag gct cat gag cag cat ctt aag tcg aag agt 291																
Gly	Tyr	Arg	Ser	Ser	Lys	Ala	His	Glu	Gln	His	Leu	Lys	Ser	Lys	Ser	
					80					85					90	
cat gtt ttg aag gct tcg acg agt act gga gag gag gat aaa gcg atc 339																
His	Val	Leu	Lys	Ala	Ser	Thr	Ser	Thr	Gly	Glu	Glu	Glu	Asp	Lys	Ala	Ile
					95			100						105		

atc aag cag ctt ccg cct cgt cgt gtt gag aag aat aac act gct caa 387
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ttg aag ggt tcg att gag gag gaa gag agt gaa gat gaa tgg att gag 435
 Leu Lys Gly Ser Ile Glu Glu Glu Glu Ser Glu Asp Glu Trp Ile Glu
 125 130 135

gtt gat tcg gat gag gat ttg gat gcg gaa atg aat gag gat ggt gaa 483
 Val Asp Ser Asp Glu Asp Leu Asp Ala Glu Met Asn Glu Asp Gly Glu
 140 145 150 155

gaa gaa gat atg gat gaa gat ggt att gaa ttt gag ttg gat ccg gct 531
 Glu Glu Asp Met Asp Glu Asp Gly Ile Glu Phe Glu Leu Asp Pro Ala
 160 165 170

tgt tgt ttg atg tgt gat aag aag cat aag act ata gag aaa tgt atg 579
 Cys Cys Leu Met Cys Asp Lys Lys His Lys Thr Ile Glu Lys Cys Met
 175 180 185

gtt cat atg cat aag ttt cat ggg ttc ttc att cct gat att gag tac 627
 Val His Met His Lys Phe His Gly Phe Phe Ile Pro Asp Ile Glu Tyr
 190 195 200

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 205 210 215

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 Arg Asp Phe Val Cys Leu Tyr Cys Asn Glu Leu Cys His Pro Phe Ser
 220 225 230 235

agt ttg gaa gct gtt cgt aag cat atg gac gcc aaa ggt cat tgc aaa 771
 Ser Leu Glu Ala Val Arg Lys His Met Asp Ala Lys Gly His Cys Lys
 240 245 250

gtg cat tat ggt gat ggt ggt gat gaa gaa gat gca gaa ctt gaa gag 819
 Val His Tyr Gly Asp Gly Gly Asp Glu Glu Asp Ala Glu Leu Glu Glu
 255 260 265

ttc tat gac tac agc agc agc tat gtc aat gga gac gaa aat cag atg 867
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 270 275 280

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 Val Val Ser Gly Glu Ser Val Asn Thr Val Glu Leu Phe Gly Gly Ser
 285 290 295

gag ctt gtg atc acc aag aga acc gat aac aaa gta acg tct agg act 963
 Glu Leu Val Ile Thr Lys Arg Thr Asp Asn Lys Val Thr Ser Arg Thr
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ctt ggg tct cga gaa ttc atg cgc tac tac aaa cag aag cca gca ccg 1011
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 320 325 330

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 335 340 345

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 350 355 360

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 365 370 375

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tctgttttgt ctgatttagt cttttgaaaa tgttacgttt tggtgagtt tgtatctctt 1383

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 35 40 45

Ala Arg Gln Ala Ala Ile Ala Gln Glu Lys Val Lys Ala Val Glu Ala
 50 55 60

Pro Met Leu Tyr Ser Cys Gly Ile Cys Asn Lys Gly Tyr Arg Ser Ser
 65 70 75 80

Lys Ala His Glu Gln His Leu Lys Ser Lys Ser His Val Leu Lys Ala
 85 90 95

Ser Thr Ser Thr Gly Glu Glu Asp Lys Ala Ile Ile Lys Gln Leu Pro
 100 105 110

CCCTGTTGCT CCTCGATTTT CAGGTCTCTC CTCTTTGTTC GATTTTGTGA CCAGAGTTTC

Pro Arg Arg Val Glu Lys Asn Asn Thr Ala Gln Leu Lys Gly Ser Ile
 115 120 125
 Glu Glu Glu Glu Ser Glu Asp Glu Trp Ile Glu Val Asp Ser Asp Glu
 130 135 140
 Asp Leu Asp Ala Glu Met Asn Glu Asp Gly Glu Glu Glu Asp Met Asp
 145 150 155 160
 Glu Asp Gly Ile Glu Phe Glu Leu Asp Pro Ala Cys Cys Leu Met Cys
 165 170 175
 Asp Lys Lys His Lys Thr Ile Glu Lys Cys Met Val His Met His Lys
 180 185 190
 Phe His Gly Phe Phe Ile Pro Asp Ile Glu Tyr Leu Lys Asp Pro Lys
 195 200 205
 Gly Phe Leu Thr Tyr Leu Gly Leu Lys Val Lys Arg Asp Phe Val Cys
 210 215 220
 Leu Tyr Cys Asn Glu Leu Cys His Pro Phe Ser Ser Leu Glu Ala Val
 225 230 235 240
 Arg Lys His Met Asp Ala Lys Gly His Cys Lys Val His Tyr Gly Asp
 245 250 255
 Gly Gly Asp Glu Glu Asp Ala Glu Leu Glu Glu Phe Tyr Asp Tyr Ser
 260 265 270
 Ser Ser Tyr Val Asn Gly Asp Glu Asn Gln Met Val Val Ser Gly Glu
 275 280 285
 Ser Val Asn Thr Val Glu Leu Phe Gly Gly Ser Glu Leu Val Ile Thr
 290 295 300
 Lys Arg Thr Asp Asn Lys Val Thr Ser Arg Thr Leu Gly Ser Arg Glu
 305 310 315 320
 Phe Met Arg Tyr Tyr Lys Gln Lys Pro Ala Pro Ser Ser Gln Lys His
 325 330 335
 Ile Val Asn Ser Leu Thr Ser Arg Tyr Lys Met Met Gly Leu Ala Thr
 340 345 350
 Val Gln Ser Lys Glu Ala Ile Val Arg Met Lys Val Met Arg Glu Met
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Asn Val Cys Asp Lys Thr Val Tyr Val Val Asp Met Leu Ser Ile Glu
                        15                      20                      25

gga atg cct tac cac aag tct tgc ttc agg tgt acc cat tgc aaa gga 149
Gly Met Pro Tyr His Lys Ser Cys Phe Arg Cys Thr His Cys Lys Gly
                        30                      35                      40

acc ctt cag atg agc aac tat tcc tcc atg gat gga gtt ttg tac tgc 197
Thr Leu Gln Met Ser Asn Tyr Ser Ser Met Asp Gly Val Leu Tyr Cys
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aag act cat ttt gag caa ctc ttc aag gaa tct ggc aat ttc agc aaa 245
Lys Thr His Phe Glu Gln Leu Phe Lys Glu Ser Gly Asn Phe Ser Lys
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aac ttt caa cca gga aaa act gag aag cca gag ctg act agg act ccc 293
Asn Phe Gln Pro Gly Lys Thr Glu Lys Pro Glu Leu Thr Arg Thr Pro
                        75                      80                      85                      90

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Ser Lys Ile Ser Ser Ile Phe Cys Gly Thr Gln Asp Lys Cys Ala Ala
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tgc gaa aaa act gtt tac cct ctt gaa aag ata caa atg gaa gga gaa 389
Cys Glu Lys Thr Val Tyr Pro Leu Glu Lys Ile Gln Met Glu Gly Glu
                        110                      115                      120

tgc ttc cac aag aca tgt ttc cgg tgc gct cac ggt ggg tgt acg ctg 437
Cys Phe His Lys Thr Cys Phe Arg Cys Ala His Gly Gly Cys Thr Leu
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Thr His Ser Ser Tyr Ala Ser Leu Asp Ser Val Leu Tyr Cys Arg His
                        140                      145                      150

cac ttt aac caa ctc ttc atg gag aaa gga aac tac gct cac gtc ctc 533
His Phe Asn Gln Leu Phe Met Glu Lys Gly Asn Tyr Ala His Val Leu
                        155                      160                      165                      170

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Gln Ala Ala Asn His Arg Arg Thr Ala Ser Gly Asn Thr Leu Pro Pro
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 Glu Pro Thr Glu Asp Val Ala Val Glu Ala Lys Glu Glu Asn Gly Val
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 Ser Glu Ser
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 35 40 45

Tyr Ser Ser Met Asp Gly Val Leu Tyr Cys Lys Thr His Phe Glu Gln
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Leu Phe Lys Glu Ser Gly Asn Phe Ser Lys Asn Phe Gln Pro Gly Lys
 65 70 75 80

Thr Glu Lys Pro Glu Leu Thr Arg Thr Pro Ser Lys Ile Ser Ser Ile
 85 90 95

Phe Cys Gly Thr Gln Asp Lys Cys Ala Ala Cys Glu Lys Thr Val Tyr
 100 105 110

Pro Leu Glu Lys Ile Gln Met Glu Gly Glu Cys Phe His Lys Thr Cys
 115 120 125

Phe Arg Cys Ala His Gly Gly Cys Thr Leu Thr His Ser Ser Tyr Ala
 130 135 140

Ser Leu Asp Ser Val Leu Tyr Cys Arg His His Phe Asn Gln Leu Phe
 145 150 155 160

Met Glu Lys Gly Asn Tyr Ala His Val Leu Gln Ala Ala Asn His Arg
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Arg Thr Ala Ser Gly Asn Thr Leu Pro Pro Glu Pro Thr Glu Asp Val
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629 678 738 760

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 195 200 205

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 Val Ile Gly Phe Phe Arg Asp Met Val Asp Ala Leu Cys Pro Tyr Ile
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 Gly Leu Pro Ser Phe Leu Asp His Asn Glu Thr Ser Gly Pro Asp Pro
 40 45 50

acc cga cac gct ctc tct acg tca gcg agt ctt gct aac gag ttg atc 246
 Thr Arg His Ala Leu Ser Thr Ser Ala Ser Leu Ala Asn Glu Leu Ile
 55 60 65 70

ccg gtg gtt cgg ttc tcg gat ctt ccg acc gat ccg gaa gat tgt tgt 294
 Pro Val Val Arg Phe Ser Asp Leu Pro Thr Asp Pro Glu Asp Cys Cys
 75 80 85

acg gtt tgt ttg tca gat ttt gag tcc gac gat aag gtt agg cag cta 342
 Thr Val Cys Leu Ser Asp Phe Glu Ser Asp Asp Lys Val Arg Gln Leu
 90 95 100

ccc aag tgt gga cac gtg ttt cat cat cat tgt tta gac cgt tgg atc 390
 Pro Lys Cys Gly His Val Phe His His His Cys Leu Asp Arg Trp Ile
 105 110 115

gtt gac tac aac aag atg aaa tgt ccg gtt tgt cgg cac cgg ttc tta 438
 Val Asp Tyr Asn Lys Met Lys Cys Pro Val Cys Arg His Arg Phe Leu
 120 125 130

ccg aaa gaa aag tac acg caa tgt gat tgg ggt tct ggt tca gat tgg 486
 Pro Lys Glu Lys Tyr Thr Gln Cys Asp Trp Gly Ser Gly Ser Asp Trp
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Ala	Leu	Cys	Pro	Tyr	Ile	Gly	Leu	Pro	Ser	Phe	Leu	Asp	His	Asn	Glu
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Asp	Pro	Glu	Asp	Cys	Cys	Thr	Val	Cys	Leu	Ser	Asp	Phe	Glu	Ser	Asp
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Asp	Lys	Val	Arg	Gln	Leu	Pro	Lys	Cys	Gly	His	Val	Phe	His	His	His
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Cys	Leu	Asp	Arg	Trp	Ile	Val	Asp	Tyr	Asn	Lys	Met	Lys	Cys	Pro	Val
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Cys	Arg	His	Arg	Phe	Leu	Pro	Lys	Glu	Lys	Tyr	Thr	Gln	Cys	Asp	Trp
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agactttgta taca atg atg aaa agt ttg gcg aat gct gtt gga gcg aag 170
Met Met Lys Ser Leu Ala Asn Ala Val Gly Ala Lys
1 5 10
acg gcg agg gct tgc gac agc tgc gtg aag aga cgt gca cgg tgg tac 218
Thr Ala Arg Ala Cys Asp Ser Cys Val Lys Arg Arg Ala Arg Trp Tyr
15 20 25
tgc gcg gcc gac gat gct ttt ctt tgc cag tct tgc gac agt ttg gtc 266
Cys Ala Ala Asp Asp Ala Phe Leu Cys Gln Ser Cys Asp Ser Leu Val
30 35 40
cat tca gca aac cct ctt gct cgc cgc cac gag aga gtc cgt ttg aag 314
His Ser Ala Asn Pro Leu Ala Arg Arg His Glu Arg Val Arg Leu Lys
45 50 55 60
acg gct agc ccg gcg gtc gta aag cat agc aac cac tca tca gct tct 362
Thr Ala Ser Pro Ala Val Val Lys His Ser Asn His Ser Ser Ala Ser
65 70 75
cct cca cat gag gtc gcc acg tgg cat cac ggg ttt act cgt aaa gct 410
Pro Pro His Glu Val Ala Thr Trp His His Gly Phe Thr Arg Lys Ala
80 85 90
cga acg cca cgt ggc tct ggt aag aaa aac aat tcg tcg ata ttt cat 458
Arg Thr Pro Arg Gly Ser Gly Lys Lys Asn Asn Ser Ser Ile Phe His
95 100 105
gac ttg gtt cct gat att agt att gag gat cag aca gac aac tat gag 506
Asp Leu Val Pro Asp Ile Ser Ile Glu Asp Gln Thr Asp Asn Tyr Glu
110 115 120
ctt gaa gag cag ctg atc tgt caa gtg ccg gtt cta gat ccg ttg gtg 554
Leu Glu Glu Gln Leu Ile Cys Gln Val Pro Val Leu Asp Pro Leu Val
125 130 135 140
tct gag cag ttc ttg aac gat gtc gtt gag ccc aag atc gag ttt cct 602
Ser Glu Gln Phe Leu Asn Asp Val Val Glu Pro Lys Ile Glu Phe Pro
145 150 155
atg atc aga agt ggt ttg atg atc gag gag gag gaa gac aac gct gaa 650
Met Ile Arg Ser Gly Leu Met Ile Glu Glu Glu Glu Asp Asn Ala Glu
160 165 170
agt tgt ctt aat gga ttt ttc ccg acc gac atg gag ctt gag gag ttt 698
Ser Cys Leu Asn Gly Phe Phe Pro Thr Asp Met Glu Leu Glu Glu Phe
175 180 185
gct gct gac gtg gag act ctg ctc ggt cgc ggg tta gac acg gag tcg 746
Ala Ala Asp Val Glu Thr Leu Leu Gly Arg Gly Leu Asp Thr Glu Ser
190 195 200

054545505454550

tat gcc atg gag gag cta ggg tta tct aat tca gag atg ttc aaa atc 794
 Tyr Ala Met Glu Glu Leu Gly Leu Ser Asn Ser Glu Met Phe Lys Ile
 205 210 215 220

gaa aaa gat gag att gaa gaa gaa gta gaa gag ata aaa gcc atg agc 842
 Glu Lys Asp Glu Ile Glu Glu Glu Val Glu Glu Ile Lys Ala Met Ser
 225 230 235

atg gat ata ttt gat gat gat cga aaa gac gtg gat gga aca gta ccg 890
 Met Asp Ile Phe Asp Asp Asp Arg Lys Asp Val Asp Gly Thr Val Pro
 240 245 250

ttt gag cta agc ttt gat tac gag tcg tca cac aag acg tcc gaa gaa 938
 Phe Glu Leu Ser Phe Asp Tyr Glu Ser Ser His Lys Thr Ser Glu Glu
 255 260 265

gag gta atg aag aac gtt gaa agt agt ggt gaa tgt gtt gtt aag gtg 986
 Glu Val Met Lys Asn Val Glu Ser Ser Gly Glu Cys Val Val Lys Val
 270 275 280

aaa gag gaa gaa cat aag aat gtt ctg atg cta aga tta aac tat gac 1034
 Lys Glu Glu Glu His Lys Asn Val Leu Met Leu Arg Leu Asn Tyr Asp
 285 290 295 300

tcg gtg ata tcc act tgg gga ggt caa ggt cca ccg tgg agt tca gga 1082
 Ser Val Ile Ser Thr Trp Gly Gly Gln Gly Pro Pro Trp Ser Ser Gly
 305 310 315

gag cca ccg gaa cga gac atg gac atc agc ggt tgg cca gcc ttt tcc 1130
 Glu Pro Pro Glu Arg Asp Met Asp Ile Ser Gly Trp Pro Ala Phe Ser
 320 325 330

atg gtg gag aat gga gga gaa agt act cat cag aag caa tac gtt ggt 1178
 Met Val Glu Asn Gly Gly Glu Ser Thr His Gln Lys Gln Tyr Val Gly
 335 340 345

gga tgt tta cca tca agt ggg ttt gga gat gga ggt aga gaa gct aga 1226
 Gly Cys Leu Pro Ser Ser Gly Phe Gly Asp Gly Gly Arg Glu Ala Arg
 350 355 360

gtt tcg aga tac aga gag aag agg agg aca agg ttg ttt tct aag aag 1274
 Val Ser Arg Tyr Arg Glu Lys Arg Arg Thr Arg Leu Phe Ser Lys Lys
 365 370 375 380

ata cgg tac gag gta cgt aaa ttg aat gca gag aaa aga cca cga atg 1322
 Ile Arg Tyr Glu Val Arg Lys Leu Asn Ala Glu Lys Arg Pro Arg Met
 385 390 395

aaa gga aga ttc gtg aag aga gcc tcg ctc gct gct gct gct tca cca 1370
 Lys Gly Arg Phe Val Lys Arg Ala Ser Leu Ala Ala Ala Ser Pro
 400 405 410

tta ggt gtt aat tac tgaatagtta atatctattc atgttatatc tcactttaca 1425
 Leu Gly Val Asn Tyr
 415

aatttcggtg aatctttttt cttctgaaac aacagaagtt attttggcac ttaattgtgc 1485

tttgaggact tgtatgtaca tagaagtaac caataataat gtgactttta ctaaaaaaaaa 1545
 aaaaaaaaaa 1554

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 Asp Ala Phe Leu Cys Gln Ser Cys Asp Ser Leu Val His Ser Ala Asn
 35 40 45
 Pro Leu Ala Arg Arg His Glu Arg Val Arg Leu Lys Thr Ala Ser Pro
 50 55 60
 Ala Val Val Lys His Ser Asn His Ser Ser Ala Ser Pro Pro His Glu
 65 70 75 80
 Val Ala Thr Trp His His Gly Phe Thr Arg Lys Ala Arg Thr Pro Arg
 85 90 95
 Gly Ser Gly Lys Lys Asn Asn Ser Ser Ile Phe His Asp Leu Val Pro
 100 105 110
 Asp Ile Ser Ile Glu Asp Gln Thr Asp Asn Tyr Glu Leu Glu Glu Gln
 115 120 125
 Leu Ile Cys Gln Val Pro Val Leu Asp Pro Leu Val Ser Glu Gln Phe
 130 135 140
 Leu Asn Asp Val Val Glu Pro Lys Ile Glu Phe Pro Met Ile Arg Ser
 145 150 155 160
 Gly Leu Met Ile Glu Glu Glu Glu Asp Asn Ala Glu Ser Cys Leu Asn
 165 170 175
 Gly Phe Phe Pro Thr Asp Met Glu Leu Glu Glu Phe Ala Ala Asp Val
 180 185 190
 Glu Thr Leu Leu Gly Arg Gly Leu Asp Thr Glu Ser Tyr Ala Met Glu
 195 200 205
 Glu Leu Gly Leu Ser Asn Ser Glu Met Phe Lys Ile Glu Lys Asp Glu
 210 215 220
 Ile Glu Glu Glu Val Glu Glu Ile Lys Ala Met Ser Met Asp Ile Phe
 225 230 235 240

Asp Asp Asp Arg Lys Asp Val Asp Gly Thr Val Pro Phe Glu Leu Ser
245 250 255

Phe Asp Tyr Glu Ser Ser His Lys Thr Ser Glu Glu Glu Val Met Lys
260 265 270

Asn Val Glu Ser Ser Gly Glu Cys Val Val Lys Val Lys Glu Glu Glu
275 280 285

His Lys Asn Val Leu Met Leu Arg Leu Asn Tyr Asp Ser Val Ile Ser
290 295 300

Thr Trp Gly Gly Gln Gly Pro Pro Trp Ser Ser Gly Glu Pro Pro Glu
305 310 315 320

Arg Asp Met Asp Ile Ser Gly Trp Pro Ala Phe Ser Met Val Glu Asn
325 330 335

Gly Gly Glu Ser Thr His Gln Lys Gln Tyr Val Gly Gly Cys Leu Pro
340 345 350

Ser Ser Gly Phe Gly Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr
355 360 365

Arg Glu Lys Arg Arg Thr Arg Leu Phe Ser Lys Lys Ile Arg Tyr Glu
370 375 380

Val Arg Lys Leu Asn Ala Glu Lys Arg Pro Arg Met Lys Gly Arg Phe
385 390 395 400

Val Lys Arg Ala Ser Leu Ala Ala Ala Ala Ser Pro Leu Gly Val Asn
405 410 415

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<223> G1258

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tcttcaagca acttctcaga ttcagctctt atg gat cat ttg tta caa cac cag 114
Met Asp His Leu Leu Gln His Gln
1 5

gat gtt ttt ggg aat tat aac aaa gca aga gaa gca atg gga cta tca 162
Asp Val Phe Gly Asn Tyr Asn Lys Ala Arg Glu Ala Met Gly Leu Ser
10 15 20

tat tca tca aac cca aca ccg tta gat aac gac cag aag aaa cct tct	210
Tyr Ser Ser Asn Pro Thr Pro Leu Asp Asn Asp Gln Lys Lys Pro Ser	
25 30 35 40	
cct gca acg gct gtg aca agg cca cag cct ccg gag cta gct ctc agg	258
Pro Ala Thr Ala Val Thr Arg Pro Gln Pro Pro Glu Leu Ala Leu Arg	
45 50 55	
tgt cca cgt tgc gac tca aca aac aca aag ttt tgt tac tac aac aac	306
Cys Pro Arg Cys Asp Ser Thr Asn Thr Lys Phe Cys Tyr Tyr Asn Asn	
60 65 70	
tac agt ctc act cag cct cgc tac ttc tgc aaa tca tgc cgg aga tat	354
Tyr Ser Leu Thr Gln Pro Arg Tyr Phe Cys Lys Ser Cys Arg Arg Tyr	
75 80 85	
tgg act aaa ggt gga act cta agg aac atc ccc gtg ggt gga ggc tgc	402
Trp Thr Lys Gly Gly Thr Leu Arg Asn Ile Pro Val Gly Gly Gly Cys	
90 95 100	
cgg aaa aac aaa cga tcc aca tct tcg gct gca aga agc ctc aga acc	450
Arg Lys Asn Lys Arg Ser Thr Ser Ser Ala Ala Arg Ser Leu Arg Thr	
105 110 115 120	
act cca gaa ccg gcg tcc cac gac ggg aaa gtc ttc tcg gcg gca ggt	498
Thr Pro Glu Pro Ala Ser His Asp Gly Lys Val Phe Ser Ala Ala Gly	
125 130 135	
ttt aat ggg tat agt aac aat gaa cat att gat ctg agc tta gcc ttt	546
Phe Asn Gly Tyr Ser Asn Asn Glu His Ile Asp Leu Ser Leu Ala Phe	
140 145 150	
gcc ttg ctg aac aaa caa cat ccg ggg agt tct tca cag cta ggg ttt	594
Ala Leu Leu Asn Lys Gln His Pro Gly Ser Ser Ser Gln Leu Gly Phe	
155 160 165	
cat tca gaa ctc ggt agc tct cat cag tct gac atg gaa ggt atg ttt	642
His Ser Glu Leu Gly Ser Ser His Gln Ser Asp Met Glu Gly Met Phe	
170 175 180	
ggg aca agc caa caa aaa gag aac gct act tat gcg ttt ggt aac ggg	690
Gly Thr Ser Gln Gln Lys Glu Asn Ala Thr Tyr Ala Phe Gly Asn Gly	
185 190 195 200	
agc agc ggt ttg ggt gat cca agc aga gtc tta tgg gga ttt cca tgg	738
Ser Ser Gly Leu Gly Asp Pro Ser Arg Val Leu Trp Gly Phe Pro Trp	
205 210 215	
cag atg aat gga gag agc ttt gga atg atg aac ata gga gga ggt ggt	786
Gln Met Asn Gly Glu Ser Phe Gly Met Met Asn Ile Gly Gly Gly Gly	
220 225 230	
ggt cat gta gat cag att gat tca ggg aga gag atg tgg acc aat atg	834
Gly His Val Asp Gln Ile Asp Ser Gly Arg Glu Met Trp Thr Asn Met	
235 240 245	

aac tac att aat tct ggt gct tta atg tagttcaaaa ttaaaacccc 881
 Asn Tyr Ile Asn Ser Gly Ala Leu Met
 250 255

aatattatattt ggggttttgat ttaggggtttg aatttcattgt tttttaatgg gagtagaaaa 941
 ggggtggtagc tattttatga aatgggttaag gaagtataga tatattaggg cttcttcaaaa 1001
 gagtttcaaaa cttgcaaaat ggggttgagg tagttcttgt tttcgatttc tgatctaaat 1061
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 taaaaaaaaa aaaaaaaaaa 1140

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 20 25 30

Asp Asn Asp Gln Lys Lys Pro Ser Pro Ala Thr Ala Val Thr Arg Pro
 35 40 45

Gln Pro Pro Glu Leu Ala Leu Arg Cys Pro Arg Cys Asp Ser Thr Asn
 50 55 60

Thr Lys Phe Cys Tyr Tyr Asn Asn Tyr Ser Leu Thr Gln Pro Arg Tyr
 65 70 75 80

Phe Cys Lys Ser Cys Arg Arg Tyr Trp Thr Lys Gly Gly Thr Leu Arg
 85 90 95

Asn Ile Pro Val Gly Gly Gly Cys Arg Lys Asn Lys Arg Ser Thr Ser
 100 105 110

Ser Ala Ala Arg Ser Leu Arg Thr Thr Pro Glu Pro Ala Ser His Asp
 115 120 125

Gly Lys Val Phe Ser Ala Ala Gly Phe Asn Gly Tyr Ser Asn Asn Glu
 130 135 140

His Ile Asp Leu Ser Leu Ala Phe Ala Leu Leu Asn Lys Gln His Pro
 145 150 155 160

Gly Ser Ser Ser Gln Leu Gly Phe His Ser Glu Leu Gly Ser Ser His
 165 170 175

Gln Ser Asp Met Glu Gly Met Phe Gly Thr Ser Gln Gln Lys Glu Asn
 180 185 190

Ala Thr Tyr Ala Phe Gly Asn Gly Ser Ser Gly Leu Gly Asp Pro Ser
 195 200 205

Arg Val Leu Trp Gly Phe Pro Trp Gln Met Asn Gly Glu Ser Phe Gly
 210 215 220

Met Met Asn Ile Gly Gly Gly Gly Gly His Val Asp Gln Ile Asp Ser
 225 230 235 240

Gly Arg Glu Met Trp Thr Asn Met Asn Tyr Ile Asn Ser Gly Ala Leu
 245 250 255

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 <223> G399

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agc tta ggg ttt tca caa aat cac aat cct ctt cag atg aat ctg aat 98
 Ser Leu Gly Phe Ser Gln Asn His Asn Pro Leu Gln Met Asn Leu Asn
 15 20 25

cct aac tct tca tta tca aac aat ctc cag aga ctc cca tgg aac caa 146
 Pro Asn Ser Ser Leu Ser Asn Asn Leu Gln Arg Leu Pro Trp Asn Gln
 30 35 40

aca ttc gat cct aca tca gat ctt cgc aag ata gac gtg aac agt ttt 194
 Thr Phe Asp Pro Thr Ser Asp Leu Arg Lys Ile Asp Val Asn Ser Phe
 45 50 55 60

cca tca acg gtt aac tgc gag gaa gac aca gga gtt tcg tca cca aac 242
 Pro Ser Thr Val Asn Cys Glu Glu Asp Thr Gly Val Ser Ser Pro Asn
 65 70 75

agt acg atc tca agc acc att agc ggg aag aga agt gag aga gaa gga 290
 Ser Thr Ile Ser Ser Thr Ile Ser Gly Lys Arg Ser Glu Arg Glu Gly
 80 85 90

atc tcc gga acc ggc gtt ggc tcc ggc gac gat cac gac gag atc act 338
 Ile Ser Gly Thr Gly Val Gly Ser Gly Asp Asp His Asp Glu Ile Thr
 95 100 105

ccg gat cga ggg tac tca cgt gga acc tca gat gaa gaa gaa gac ggg 386
 Pro Asp Arg Gly Tyr Ser Arg Gly Thr Ser Asp Glu Glu Glu Asp Gly
 110 115 120

ggc gaa acg tcg agg aag aag ctc agg tta tca aaa gat cag tct gct 434
 Gly Glu Thr Ser Arg Lys Lys Leu Arg Leu Ser Lys Asp Gln Ser Ala
 125 130 135 140

ttt ctc gaa gag act ttc aaa gaa cac aac act ctc aat ccc aaa cag 482
 Phe Leu Glu Glu Thr Phe Lys Glu His Asn Thr Leu Asn Pro Lys Gln
 145 150 155

aag cta gct ttg gct aag aag ctg aac ttg acg gca aga caa gtg gaa 530
 Lys Leu Ala Leu Ala Lys Lys Leu Asn Leu Thr Ala Arg Gln Val Glu
 160 165 170

gtg tgg ttc caa aac aga aga gct agg tgagattttc ttgtcttaac 577
 Val Trp Phe Gln Asn Arg Arg Ala Arg
 175 180

accaaaattg taaaattaca ttataccctt cttgtgtaga agttttttact tacaagggtcc 637
 gatttggttt tacagaacca agttaagca aacggaggta gattgcgaat acttgaaacg 697
 gtgcgtagag aagctaacgg aagagaaccg gagacttcag aaagaggcta tggagcttcg 757
 aactctcaag ctgtctccac aattctacgg tcagatgact ccaccaacta cactcatcat 817
 gtgtccttcg tgcgagcgtg tgggtggccc atcatcatcg aaccatcacc acaatcacag 877
 gcccgtttct atcaatccgt ggggtgcttg tgctggtcag gtggctcatg ggctgaattt 937
 tgaagccttg cgtccacgat cgtgattttt tatttttagtg gtgggaaaag ggtgttttgg 997
 tatttttcgt tatcggtata tagtctatct gtgtggggtc attgtaattt tggatgattg 1057
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 Leu Ser Asn Asn Leu Gln Arg Leu Pro Trp Asn Gln Thr Phe Asp Pro
 35 40 45

Thr Ser Asp Leu Arg Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val
50 55 60

Asn Cys Glu Glu Asp Thr Gly Val Ser Ser Pro Asn Ser Thr Ile Ser
65 70 75 80

Ser Thr Ile Ser Gly Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr
85 90 95

Gly Val Gly Ser Gly Asp Asp His Asp Glu Ile Thr Pro Asp Arg Gly
100 105 110

Tyr Ser Arg Gly Thr Ser Asp Glu Glu Glu Asp Gly Gly Glu Thr Ser
115 120 125

Arg Lys Lys Leu Arg Leu Ser Lys Asp Gln Ser Ala Phe Leu Glu Glu
130 135 140

Thr Phe Lys Glu His Asn Thr Leu Asn Pro Lys Gln Lys Leu Ala Leu
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Ala Lys Lys Leu Asn Leu Thr Ala Arg Gln Val Glu Val Trp Phe Gln
165 170 175

Asn Arg Arg Ala Arg
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<210> 125

<211> 1157

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<222> (3)..(884)

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act tct aca gat gaa cag agt cca aga ggg tac gga agt aat tac caa 95
Thr Ser Thr Asp Glu Gln Ser Pro Arg Gly Tyr Gly Ser Asn Tyr Gln
20 25 30

tct atg ctt gaa ggt tac gat gaa gat gct aca cta atc gag gaa tat 143
Ser Met Leu Glu Gly Tyr Asp Glu Asp Ala Thr Leu Ile Glu Glu Tyr
35 40 45

tcc ggc aac cac cac cac atg ggt cta tcg gag aag aag aga aga tta 191
Ser Gly Asn His His His Met Gly Leu Ser Glu Lys Lys Arg Arg Leu
50 55 60

aaa gtt gac caa gtc aaa gct ctt gag aag aat ttc gaa ctt gag aat 239
Lys Val Asp Gln Val Lys Ala Leu Glu Lys Asn Phe Glu Leu Glu Asn
65 70 75

aaa ctc gaa cct gag agg aaa act aaa tta gca caa gag ctt gga ctt 287
 Lys Leu Glu Pro Glu Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu
 80 85 90 95

caa cct cgt caa gta gct gtt tgg ttt cag aac cgt cgt gca cgg tgg 335
 Gln Pro Arg Gln Val Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp
 100 105 110

aaa aca aaa cag ctt gaa aaa gat tac ggt gtt ctt aag ggt caa tac 383
 Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr
 115 120 125

gat tct ctc cgc cac aat ttc gat tct ctc cgc cgt gac aat gat tcc 431
 Asp Ser Leu Arg His Asn Phe Asp Ser Leu Arg Arg Asp Asn Asp Ser
 130 135 140

ctt ctc caa gag att agt aaa atc aaa gct aag gta aac ggt gaa gaa 479
 Leu Leu Gln Glu Ile Ser Lys Ile Lys Ala Lys Val Asn Gly Glu Glu
 145 150 155

gat aac aac aac aac aaa gct att acg gag ggt gtt aag gaa gag gaa 527
 Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu Gly Val Lys Glu Glu Glu
 160 165 170 175

gtt cac aag acg gat tgc att cct tgc tct cct ctg cag ttt cta gaa 575
 Val His Lys Thr Asp Ser Ile Pro Ser Ser Pro Leu Gln Phe Leu Glu
 180 185 190

cat tcc tct ggt ttt aac tac cgg cga agc ttc act gac ctc cgt gac 623
 His Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr Asp Leu Arg Asp
 195 200 205

ctt cta ccg aat tcc acc gtt gtc gag gct gga tct tcc gat agt tgc 671
 Leu Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser Ser Asp Ser Cys
 210 215 220

gat tca agc gcc gtt ctt aac gac gaa aca agt tct gat aac gga aga 719
 Asp Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser Asp Asn Gly Arg
 225 230 235

ttg acg ccg cct gtg acg gtt act ggc ggg agt ttc tta cag ttt gtg 767
 Leu Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe Leu Gln Phe Val
 240 245 250 255

aaa aca gag caa aca gag gat cac gag gat ttt cta agc ggt gaa gaa 815
 Lys Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu Ser Gly Glu Glu
 260 265 270

gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca ctt cat tgg tac 863
 Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser Leu His Trp Tyr
 275 280 285

tct gct tca gat cat tgg act tgagaattgt ttatcaaatt ggtgctctgt 914
 Ser Ala Ser Asp His Trp Thr
 290

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			20					25					30			
Met	Leu	Glu	Gly	Tyr	Asp	Glu	Asp	Ala	Thr	Leu	Ile	Glu	Glu	Tyr	Ser	
		35					40					45				
Gly	Asn	His	His	His	Met	Gly	Leu	Ser	Glu	Lys	Lys	Arg	Arg	Leu	Lys	
	50					55					60					
Val	Asp	Gln	Val	Lys	Ala	Leu	Glu	Lys	Asn	Phe	Glu	Leu	Glu	Asn	Lys	
65					70					75					80	
Leu	Glu	Pro	Glu	Arg	Lys	Thr	Lys	Leu	Ala	Gln	Glu	Leu	Gly	Leu	Gln	
				85					90					95		
Pro	Arg	Gln	Val	Ala	Val	Trp	Phe	Gln	Asn	Arg	Arg	Ala	Arg	Trp	Lys	
			100					105					110			
Thr	Lys	Gln	Leu	Glu	Lys	Asp	Tyr	Gly	Val	Leu	Lys	Gly	Gln	Tyr	Asp	
		115					120					125				
Ser	Leu	Arg	His	Asn	Phe	Asp	Ser	Leu	Arg	Arg	Asp	Asn	Asp	Ser	Leu	
	130					135					140					
Leu	Gln	Glu	Ile	Ser	Lys	Ile	Lys	Ala	Lys	Val	Asn	Gly	Glu	Glu	Asp	
145					150					155					160	
Asn	Asn	Asn	Asn	Lys	Ala	Ile	Thr	Glu	Gly	Val	Lys	Glu	Glu	Glu	Val	
				165					170					175		
His	Lys	Thr	Asp	Ser	Ile	Pro	Ser	Ser	Pro	Leu	Gln	Phe	Leu	Glu	His	
			180					185					190			
Ser	Ser	Gly	Phe	Asn	Tyr	Arg	Arg	Ser	Phe	Thr	Asp	Leu	Arg	Asp	Leu	
		195					200					205				

Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser Ser Asp Ser Cys Asp
 210 215 220
 Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser Asp Asn Gly Arg Leu
 225 230 235 240
 Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe Leu Gln Phe Val Lys
 245 250 255
 Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu Ser Gly Glu Glu Ala
 260 265 270
 Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser Leu His Trp Tyr Ser
 275 280 285
 Ala Ser Asp His Trp Thr
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 <223> G964

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 ttcctgaaac tggtgagttc ttgtgaaagg aaataaaaaa c atg atg atg ggc aaa 176
 Met Met Met Gly Lys
 1 5
 gaa gat cta ggt ttg agc cta agc tta ggg ttt tca caa aat cac aat 224
 Glu Asp Leu Gly Leu Ser Leu Ser Leu Gly Phe Ser Gln Asn His Asn
 10 15 20
 cct ctt cag atg aat ctg aat cct aac tct tca tta tca aac aat ctc 272
 Pro Leu Gln Met Asn Leu Asn Pro Asn Ser Ser Leu Ser Asn Asn Leu
 25 30 35
 cag aga ctc cca tgg aac caa aca ttc gat cct aca tca gat ctt cgc 320
 Gln Arg Leu Pro Trp Asn Gln Thr Phe Asp Pro Thr Ser Asp Leu Arg
 40 45 50
 aag ata gac gtg aac agt ttt cca tca acg gtt aac tgc gag gaa gac 368
 Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val Asn Cys Glu Glu Asp
 55 60 65
 aca gga gtt tcg tca cca aac agt acg atc tca agc acc att agc ggg 416
 Thr Gly Val Ser Ser Pro Asn Ser Thr Ile Ser Ser Thr Ile Ser Gly
 70 75 80 85

aag aga agt gag aga gaa gga atc tcc gga acc ggc gtt ggc tcc ggc 464
Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr Gly Val Gly Ser Gly
90 95 100

gac gat cac gac gag atc act ccg gat cga ggg tac tca cgt gga acc 512
Asp Asp His Asp Glu Ile Thr Pro Asp Arg Gly Tyr Ser Arg Gly Thr
105 110 115

tca gat gaa gaa gaa gac ggg ggc gaa acg tcg agg aag aag ctc agg 560
Ser Asp Glu Glu Glu Asp Gly Gly Glu Thr Ser Arg Lys Lys Leu Arg
120 125 130

tta tca aaa gat cag tct gct ttt ctc gaa gag act ttc aaa gaa cac 608
Leu Ser Lys Asp Gln Ser Ala Phe Leu Glu Glu Thr Phe Lys Glu His
135 140 145

aac act ctc aat ccc aaa cag aag cta gct ttg gct aag aag ctg aac 656
Asn Thr Leu Asn Pro Lys Gln Lys Leu Ala Leu Ala Lys Lys Leu Asn
150 155 160 165

ttg acg gca aga caa gtg gaa gtg tgg ttc caa aac aga aga gct aga 704
Leu Thr Ala Arg Gln Val Glu Val Trp Phe Gln Asn Arg Arg Ala Arg
170 175 180

acc aag tta aag caa acg gag gta gat tgc gaa tac ttg aaa cgg tgc 752
Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu Tyr Leu Lys Arg Cys
185 190 195

gta gag aag cta acg gaa gag aac cgg aga ctt cag aaa gag gct atg 800
Val Glu Lys Leu Thr Glu Glu Asn Arg Arg Leu Gln Lys Glu Ala Met
200 205 210

gag ctt cga act ctc aag ctg tct cca caa ttc tac ggt cag atg act 848
Glu Leu Arg Thr Leu Lys Leu Ser Pro Gln Phe Tyr Gly Gln Met Thr
215 220 225

cca cca act aca ctc atc atg tgt cct tcg tgc gag cgt gta gct ggt 896
Pro Pro Thr Thr Leu Ile Met Cys Pro Ser Cys Glu Arg Val Ala Gly
230 235 240 245

cca tca tca tcg aac cat cac cac aat cac agg ccg gtt tcg att aac 944
Pro Ser Ser Ser Asn His His His Asn His Arg Pro Val Ser Ile Asn
250 255 260

ccg tgg att gct tgt gct ggt cag gtg gct cat ggg ctg aat ttt gaa 992
Pro Trp Ile Ala Cys Ala Gly Gln Val Ala His Gly Leu Asn Phe Glu
265 270 275

gcc ttg cgt cca cga tcg taatttttag tgggtggggga aggggtgtttt 1040
Ala Leu Arg Pro Arg Ser
280

gggttttttc attatcgtaa tatagtctat ctgtgtgggg tcattgtaat tttggatgat 1100

tggccttctc atgaactagt catatgtatg atgcaacctt aaaaatattt caagtagcaa 1160

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1221

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 35 40 45
 Thr Ser Asp Leu Arg Lys Ile Asp Val Asn Ser Phe Pro Ser Thr Val
 50 55 60
 Asn Cys Glu Glu Asp Thr Gly Val Ser Ser Pro Asn Ser Thr Ile Ser
 65 70 75 80
 Ser Thr Ile Ser Gly Lys Arg Ser Glu Arg Glu Gly Ile Ser Gly Thr
 85 90 95
 Gly Val Gly Ser Gly Asp Asp His Asp Glu Ile Thr Pro Asp Arg Gly
 100 105 110
 Tyr Ser Arg Gly Thr Ser Asp Glu Glu Glu Asp Gly Gly Glu Thr Ser
 115 120 125
 Arg Lys Lys Leu Arg Leu Ser Lys Asp Gln Ser Ala Phe Leu Glu Glu
 130 135 140
 Thr Phe Lys Glu His Asn Thr Leu Asn Pro Lys Gln Lys Leu Ala Leu
 145 150 155 160
 Ala Lys Lys Leu Asn Leu Thr Ala Arg Gln Val Glu Val Trp Phe Gln
 165 170 175
 Asn Arg Arg Ala Arg Thr Lys Leu Lys Gln Thr Glu Val Asp Cys Glu
 180 185 190
 Tyr Leu Lys Arg Cys Val Glu Lys Leu Thr Glu Glu Asn Arg Arg Leu
 195 200 205
 Gln Lys Glu Ala Met Glu Leu Arg Thr Leu Lys Leu Ser Pro Gln Phe
 210 215 220
 Tyr Gly Gln Met Thr Pro Pro Thr Thr Leu Ile Met Cys Pro Ser Cys
 225 230 235 240

555150 " 615160

cca ctg aag atg gag aca gaa gaa gat ggt acc atc tat gtg aac tca 495
Pro Leu Lys Met Glu Thr Glu Glu Asp Gly Thr Ile Tyr Val Asn Ser
125 130 135 140

aag cag tac cat gga att atc agg cga cgc cag tcc cga gca aag gct 543
Lys Gln Tyr His Gly Ile Ile Arg Arg Arg Gln Ser Arg Ala Lys Ala
145 150 155

gaa aaa ctg agt aga tgc cgt aag cca tat atg cat cac tca cgc cat 591
Glu Lys Leu Ser Arg Cys Arg Lys Pro Tyr Met His His Ser Arg His
160 165 170

ctc cat gct atg cgc cgt cct aga gga tct ggc ggg cgt ttc ttg aac 639
Leu His Ala Met Arg Arg Pro Arg Gly Ser Gly Gly Arg Phe Leu Asn
175 180 185

acc aag aca gct gat gcg gct aag cag tct aag ccg agt aat tct cag 687
Thr Lys Thr Ala Asp Ala Ala Lys Gln Ser Lys Pro Ser Asn Ser Gln
190 195 200

agt tct gaa gtc ttt cat ccg gaa aat gag acc ata aac tca tcg agg 735
Ser Ser Glu Val Phe His Pro Glu Asn Glu Thr Ile Asn Ser Ser Arg
205 210 215 220

gaa gca aat gag tca aat ctc tcg gat tct gca gtt aca agt atg gat 783
Glu Ala Asn Glu Ser Asn Leu Ser Asp Ser Ala Val Thr Ser Met Asp
225 230 235

tac ttt cta agt tcg tcg gct tat tct cct ggt ggc atg gtc atg cct 831
Tyr Phe Leu Ser Ser Ser Ala Tyr Ser Pro Gly Gly Met Val Met Pro
240 245 250

atc aag tgg aat gca gca gca atg gat att ggc tgc tgc aaa ctt aat 879
Ile Lys Trp Asn Ala Ala Ala Met Asp Ile Gly Cys Cys Lys Leu Asn
255 260 265

ata tgatcagcag ataggggaca agacatgatt ggtcaccagt ccttttgtct 932
Ile

tgtcccttat ctttcagcca aacggaaaga gaacttgtgt cttggaaaaa agacattgag 992

tttccttggt ttataagatt ggctccttta ccatccgttt ggctgtaaac aggcaaatca 1052

tctttggctc atgcttcac aagttcttat cttegtctgt tttctttctac gcatcttcat 1112

aagatctctg aactagttaa taacatttcc tagcatcatg tttcaactag tgtgtgttgt 1172

aagaaactct gccttatttc cagatgatgt attgtgtgta acgtgtttat gaaacaaacg 1232

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 Met Glu Cys Asn Ala Lys Pro Pro Phe Gln Trp Glu Leu Glu Asn
 1 5 10 15

ttg ata tct ttt ggc act tct aca gct gaa gtt cct aga aag cta aaa 156
 Leu Ile Ser Phe Gly Thr Ser Thr Ala Glu Val Pro Arg Lys Leu Lys
 20 25 30

cca atg gag tgg gaa att gat gga ttt gat tgc acc tct ctg tat tct 204
 Pro Met Glu Trp Glu Ile Asp Gly Phe Asp Cys Thr Ser Leu Tyr Ser
 35 40 45

tca agc ttt gcc tat gct ggt agt tca ggt tct gat ata gct cat gct 252
 Ser Ser Phe Ala Tyr Ala Gly Ser Ser Gly Ser Asp Ile Ala His Ala
 50 55 60

ttc tct aaa agc tca aag tca act tcc att agc tct tca tca gct gaa 300
 Phe Ser Lys Ser Ser Lys Ser Thr Ser Ile Ser Ser Ser Ser Ala Glu
 65 70 75

gta aga aca cac aat ttt aca tcc gaa act ggt gaa agt ctt cct gga 348
 Val Arg Thr His Asn Phe Thr Ser Glu Thr Gly Glu Ser Leu Pro Gly
 80 85 90 95

gaa ttt gca aag ggg att gat act tct cca act ctt gaa ctt tct ttt 396
 Glu Phe Ala Lys Gly Ile Asp Thr Ser Pro Thr Leu Glu Leu Ser Phe
 100 105 110

ggc tct ggt gat ccg gtt ctc ggt tta aag ctt gct aaa cga acg tac 444
 Gly Ser Gly Asp Pro Val Leu Gly Leu Lys Leu Ala Lys Arg Thr Tyr
 115 120 125

ttt gaa gac ttt tgg gaa gtg gag aat gct aaa ggt ttg gga ctt cct 492
 Phe Glu Asp Phe Trp Glu Val Glu Asn Ala Lys Gly Leu Gly Leu Pro
 130 135 140

gtg act ctc gct tca tct tct gtt tct ccc gtg aag aaa tcg aaa tcc 540
 Val Thr Leu Ala Ser Ser Ser Val Ser Pro Val Lys Lys Ser Lys Ser
 145 150 155

att cct cag acc tta caa act cct cac tgt caa gtt gaa ggc tgt aat 588
 Ile Pro Gln Thr Leu Gln Thr Pro His Cys Gln Val Glu Gly Cys Asn
 160 165 170 175

ctt gat ctt tca tca gct aaa gac tat cat cgg aaa cat agg att tgt 636
 Leu Asp Leu Ser Ser Ala Lys Asp Tyr His Arg Lys His Arg Ile Cys
 180 185 190

gaa aac cat tca aag ttt cct aaa gtc gtt gtg agt ggc gta gag cgt 684
 Glu Asn His Ser Lys Phe Pro Lys Val Val Val Ser Gly Val Glu Arg
 195 200 205

cgg ttc tgc caa caa tgt agc agg ttc cac tgt ctc tcc gag ttt gat 732
 Arg Phe Cys Gln Gln Cys Ser Arg Phe His Cys Leu Ser Glu Phe Asp
 210 215 220

gag aag aaa cgt agc tgt cgc cga cct ctc tca gat cac aat gca aga 780
 Glu Lys Lys Arg Ser Cys Arg Arg Pro Leu Ser Asp His Asn Ala Arg
 225 230 235

cgt cgc aag cca aat cct gga agg aca tat gat ggg aaa cca cag gtg 828
 Arg Arg Lys Pro Asn Pro Gly Arg Thr Tyr Asp Gly Lys Pro Gln Val
 240 245 250 255

gat ttt gta tgg aac aga ttt gca ctt atc cat cca aga agt gag gaa 876
 Asp Phe Val Trp Asn Arg Phe Ala Leu Ile His Pro Arg Ser Glu Glu
 260 265 270

aag ttt cta tgg ccc agt tca aag cct gta cca tca aga gtc tta atg 924
 Lys Phe Leu Trp Pro Ser Ser Lys Pro Val Pro Ser Arg Val Leu Met
 275 280 285

ccg cag cct gca aag acc gag att tcc aat aag ctg ttc acc gag cac 972
 Pro Gln Pro Ala Lys Thr Glu Ile Ser Asn Lys Leu Phe Thr Glu His
 290 295 300

agt aga ttt gga ttg ttg gac ccc aaa aca aaa tcc gca aga gcg gag 1020
 Ser Arg Phe Gly Leu Leu Asp Pro Lys Thr Lys Ser Ala Arg Ala Glu
 305 310 315

tta ttc agt aaa gaa aag gtc aca atc tct tca cac atg ggt gct tct 1068
 Leu Phe Ser Lys Glu Lys Val Thr Ile Ser Ser His Met Gly Ala Ser
 320 325 330 335

caa gat ctt gat ggt gct ctc tct ctt ctg tca aat tca aca aca tgg 1116
 Gln Asp Leu Asp Gly Ala Leu Ser Leu Leu Ser Asn Ser Thr Thr Trp
 340 345 350

gtt tct tcc tct gac caa cca aga cgt ttt acc ctt gat cac cat ccc 1164
 Val Ser Ser Ser Asp Gln Pro Arg Arg Phe Thr Leu Asp His His Pro
 355 360 365

tca agc aac ctc caa ccc gta gct aac cgg tct gcg gct caa ctc agt 1212
 Ser Ser Asn Leu Gln Pro Val Ala Asn Arg Ser Ala Ala Gln Leu Ser
 370 375 380

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 Ser Val Ser Gly Tyr Trp Gln Pro Asp Pro Pro Ala Val Glu Gly Pro
 385 390 395

acc gct ctg cat aga aat ggg gca ggc cag ttt aat gaa aac tac ttc 1308
 Thr Ala Leu His Arg Asn Gly Ala Gly Gln Phe Asn Glu Asn Tyr Phe
 400 405 410 415

agc ttg aac cag ttt tat aac tgaaagctgt atgccttta atcctattta 1359
 Ser Leu Asn Gln Phe Tyr Asn
 420

ggatcaagca agctagtgat aagttaagat aggagctgtg aaacttgcaa gacaccaa 1419

cctctcttat ttctttgtcc aaatattttc atgggttaga gagctttgac aattgtcttt 1479

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Met Glu Trp Glu Ile Asp Gly Phe Asp Cys Thr Ser Leu Tyr Ser Ser
35 40 45

Ser Phe Ala Tyr Ala Gly Ser Ser Gly Ser Asp Ile Ala His Ala Phe
50 55 60

Ser Lys Ser Ser Lys Ser Thr Ser Ile Ser Ser Ser Ser Ala Glu Val
65 70 75 80

Arg Thr His Asn Phe Thr Ser Glu Thr Gly Glu Ser Leu Pro Gly Glu
85 90 95

Phe Ala Lys Gly Ile Asp Thr Ser Pro Thr Leu Glu Leu Ser Phe Gly
100 105 110

Ser Gly Asp Pro Val Leu Gly Leu Lys Leu Ala Lys Arg Thr Tyr Phe
115 120 125

Glu Asp Phe Trp Glu Val Glu Asn Ala Lys Gly Leu Gly Leu Pro Val
130 135 140

Thr Leu Ala Ser Ser Ser Val Ser Pro Val Lys Lys Ser Lys Ser Ile
145 150 155 160

Pro Gln Thr Leu Gln Thr Pro His Cys Gln Val Glu Gly Cys Asn Leu
165 170 175

Asp Leu Ser Ser Ala Lys Asp Tyr His Arg Lys His Arg Ile Cys Glu
180 185 190

Asn His Ser Lys Phe Pro Lys Val Val Val Ser Gly Val Glu Arg Arg
195 200 205

Phe Cys Gln Gln Cys Ser Arg Phe His Cys Leu Ser Glu Phe Asp Glu
210 215 220

666160"616160"60

Lys Lys Arg Ser Cys Arg Arg Pro Leu Ser Asp His Asn Ala Arg Arg
225 230 235 240

Arg Lys Pro Asn Pro Gly Arg Thr Tyr Asp Gly Lys Pro Gln Val Asp
245 250 255

Phe Val Trp Asn Arg Phe Ala Leu Ile His Pro Arg Ser Glu Glu Lys
260 265 270

Phe Leu Trp Pro Ser Ser Lys Pro Val Pro Ser Arg Val Leu Met Pro
275 280 285

Gln Pro Ala Lys Thr Glu Ile Ser Asn Lys Leu Phe Thr Glu His Ser
290 295 300

Arg Phe Gly Leu Leu Asp Pro Lys Thr Lys Ser Ala Arg Ala Glu Leu
305 310 315 320

Phe Ser Lys Glu Lys Val Thr Ile Ser Ser His Met Gly Ala Ser Gln
325 330 335

Asp Leu Asp Gly Ala Leu Ser Leu Leu Ser Asn Ser Thr Thr Trp Val
340 345 350

Ser Ser Ser Asp Gln Pro Arg Arg Phe Thr Leu Asp His His Pro Ser
355 360 365

Ser Asn Leu Gln Pro Val Ala Asn Arg Ser Ala Ala Gln Leu Ser Ser
370 375 380

Val Ser Gly Tyr Trp Gln Pro Asp Pro Pro Ala Val Glu Gly Pro Thr
385 390 395 400

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Gly Val Leu Arg Leu Pro Gly Phe Arg Phe His Pro Thr Asp Glu
10 15 20 25

gaa ctt gtg gtt caa tac ctt aag agg aaa gtt tgt tct tct cct ttg	147
Glu Leu Val Val Gln Tyr Leu Lys Arg Lys Val Cys Ser Ser Pro Leu	
30 35 40	
cca gct tca atc atc cct gag ttt gat gtt tgc aga gct gat cct tgg	195
Pro Ala Ser Ile Ile Pro Glu Phe Asp Val Cys Arg Ala Asp Pro Trp	
45 50 55	
gat tta cct cgc aat ttg gag aaa gag agg tac ttc ttt agc aca agg	243
Asp Leu Pro Arg Asn Leu Glu Lys Glu Arg Tyr Phe Phe Ser Thr Arg	
60 65 70	
gaa gct aaa tac cca aat ggg aac cgg tct aac cgg gca act ggg tct	291
Glu Ala Lys Tyr Pro Asn Gly Asn Arg Ser Asn Arg Ala Thr Gly Ser	
75 80 85	
ggg tat tgg aaa gct acc ggt att gat aaa cgg gtt gtg acc tct aga	339
Gly Tyr Trp Lys Ala Thr Gly Ile Asp Lys Arg Val Val Thr Ser Arg	
90 95 100 105	
gga aat caa atc gtt ggt ttg aag aaa act ctt gtc ttc tac aaa ggc	387
Gly Asn Gln Ile Val Gly Leu Lys Lys Thr Leu Val Phe Tyr Lys Gly	
110 115 120	
aaa cca cct cat ggc tca aga acc gat tgg atc atg cac gaa tat cgc	435
Lys Pro Pro His Gly Ser Arg Thr Asp Trp Ile Met His Glu Tyr Arg	
125 130 135	
ctc tct tct tct cct ccg agt tct atg ggt ccc act cag aac tgg gta	483
Leu Ser Ser Ser Pro Pro Ser Ser Met Gly Pro Thr Gln Asn Trp Val	
140 145 150	
ctc tgt cgt atc ttc ttg aag aaa aga gcc ggt aac aag aac gac gac	531
Leu Cys Arg Ile Phe Leu Lys Lys Arg Ala Gly Asn Lys Asn Asp Asp	
155 160 165	
gac gac gga gat agc cgt aat ctt aga cat aat aat aat aac aat tcg	579
Asp Asp Gly Asp Ser Arg Asn Leu Arg His Asn Asn Asn Asn Asn Ser	
170 175 180 185	
agt gac caa att gag ata att aca aca gac caa aca gat gat aaa aca	627
Ser Asp Gln Ile Glu Ile Ile Thr Thr Asp Gln Thr Asp Asp Lys Thr	
190 195 200	
aaa cca atc ttc ttt gat ttc atg aga aaa gaa aga aca aca gat ttg	675
Lys Pro Ile Phe Phe Asp Phe Met Arg Lys Glu Arg Thr Thr Asp Leu	
205 210 215	
aac ctt ttg ccg agc tct cct tct tcc gat cat gct tca agt gga gtc	723
Asn Leu Leu Pro Ser Ser Pro Ser Asp His Ala Ser Ser Gly Val	
220 225 230	
acg acg gag atc ttc tct tct tcc gat gaa gag acc agt agt tgc aat	771
Thr Thr Glu Ile Phe Ser Ser Ser Asp Glu Glu Thr Ser Ser Cys Asn	
235 240 245	

820

880

885

Thr Thr Asp Gln Thr Asp Asp Lys Thr Lys Pro Ile Phe Phe Asp Phe
195 200 205

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						1	5						10				
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Thr	Glu	Leu	Arg	Leu	Gly	Leu	Pro	Gly	Arg	Asp	Val	Ala	Glu	Lys	Met		
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atg	aag	aag	aga	gct	ttc	acg	gag	atg	aat	atg	acg	tcg	tcg	ggg	agt	147	
Met	Lys	Lys	Arg	Ala	Phe	Thr	Glu	Met	Asn	Met	Thr	Ser	Ser	Gly	Ser		
			30	35						40							
aat	agt	gat	caa	tgt	gaa	agc	ggc	gtc	gtt	tca	tct	ggg	ggg	gac	gct	195	
Asn	Ser	Asp	Gln	Cys	Glu	Ser	Gly	Val	Val	Ser	Ser	Gly	Gly	Asp	Ala		
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Glu	Lys	Val	Asn	Asp	Ser	Pro	Ala	Ala	Lys	Ser	Gln	Val	Val	Gly	Trp		
		60	65						70								
cca	ccg	gtt	tgt	tct	tac	cgg	aag	aaa	aac	agc	tgt	aag	gaa	gct	tcg	291	
Pro	Pro	Val	Cys	Ser	Tyr	Arg	Lys	Lys	Asn	Ser	Cys	Lys	Glu	Ala	Ser		
75		80						85						90			
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Thr	Thr	Lys	Val	Gly	Leu	Gly	Tyr	Val	Lys	Val	Ser	Met	Asp	Gly	Val		
				95	100						105						
cct	tat	ttg	agg	aag	atg	gat	ctt	ggg	tcg	agc	caa	ggc	tat	gat	gat	387	
Pro	Tyr	Leu	Arg	Lys	Met	Asp	Leu	Gly	Ser	Ser	Gln	Gly	Tyr	Asp	Asp		
			110	115						120							
cta	gcc	ttt	gct	ctt	gat	aag	ctc	ttc	ggg	ttc	cgt	ggc	atc	ggg	gtg	435	
Leu	Ala	Phe	Ala	Leu	Asp	Lys	Leu	Phe	Gly	Phe	Arg	Gly	Ile	Gly	Val		
		125	130						135								

Lys Leu Phe Gly Phe Arg Gly Ile Gly Val Ala Leu Lys Asp Gly Asp
130 135 140

Asn Cys Glu Tyr Val Thr Ile Tyr Glu Asp Lys Asp Gly Asp Trp Met
145 150 155 160

Leu Ala Gly Asp Val Pro Trp Gly Met Phe Leu Glu Ser Cys Lys Arg
165 170 175

Leu Arg Ile Met Lys Arg Ser Asp Ala Thr Gly Phe Gly Leu Gln Pro
180 185 190

Arg Gly Val Asp Glu
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<222> (186)..(1037)

<223> G782

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tcaatttgat cgtcctgaat tcacgtcct atttaggggtt tcgatcaciaa tctgaagagg 180

aggtc atg gac gtt tct gct aga aag tca caa aaa gct ggg cgc gaa aag 230

Met Asp Val Ser Ala Arg Lys Ser Gln Lys Ala Gly Arg Glu Lys
1 5 10 15

ttg agg agg gaa aaa ctg aat gag cat ttt gtt gaa ctg gga aat gta 278

Leu Arg Arg Glu Lys Leu Asn Glu His Phe Val Glu Leu Gly Asn Val
20 25 30

ctc gat cca gag aga ccc aag aat gac aaa gcc acg att ctg act gat 326

Leu Asp Pro Glu Arg Pro Lys Asn Asp Lys Ala Thr Ile Leu Thr Asp
35 40 45

act gtt cag ttg ttg aaa gag ctc aca tct gaa gtc aac aaa ctg aaa 374

Thr Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys
50 55 60

tct gag tac acc gca ttg aca gat gag tcc cgc gag ttg aca cag gag 422

Ser Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu
65 70 75

aaa aac gac ctg aga gaa gaa aag aca tcg ctg aaa tca gat ata gag 470

Lys Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu
80 85 90 95

aat ctc aat ctt caa tac cag cag aga tta agg tca atg tct cca tgg 518

Asn Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp
100 105 110

gga gct gcg atg gat cac aca gtc atg atg gct cca cca ccc tcc ttt 566
 Gly Ala Ala Met Asp His Thr Val Met Met Ala Pro Pro Pro Ser Phe
 115 120 125

cca tac cct atg cct att gct atg cct ccc ggg tca atc cca atg cat 614
 Pro Tyr Pro Met Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His
 130 135 140

cca tca atg cca tct tac aca tac ttt ggg aac cag aac cct agc atg 662
 Pro Ser Met Pro Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met
 145 150 155

atc cca gct cca tgt cct aca tac atg ccc tac atg cct cct aat aca 710
 Ile Pro Ala Pro Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr
 160 165 170 175

gtc gtt gag caa caa tcc gtg cac att cca cag aac ccc ggt aac cgt 758
 Val Val Glu Gln Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg
 180 185 190

tct cgg gaa cct aga gca aag gtt tca aga gag agc aga tct gag aaa 806
 Ser Arg Glu Pro Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys
 195 200 205

gca gag gac tcc aac gaa gtt gca aca caa ctc gaa tta aaa acc cct 854
 Ala Glu Asp Ser Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro
 210 215 220

gga tct act tct gat aag gat aca ttg caa agg cca gag aag aca aag 902
 Gly Ser Thr Ser Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys
 225 230 235

aga tgt aag aga aac aac aac aac aac tca ata gaa gaa agc tct cat 950
 Arg Cys Lys Arg Asn Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His
 240 245 250 255

tct agc aag tgt tca tct tct ccg agc gta cga gac cac agt tct tcc 998
 Ser Ser Lys Cys Ser Ser Ser Pro Ser Val Arg Asp His Ser Ser Ser
 260 265 270

agt agc gta gct ggt ggc caa aaa cct gat gat gca aaa tgattcgaaa 1047
 Ser Ser Val Ala Gly Gly Gln Lys Pro Asp Asp Ala Lys
 275 280

gaatctgatg ttgatcatct caagtatcca agtatcgttt cgatgagtac tgtatatagt 1107

gcgagtacaa aatgcactta gctgtttaaa gcagtgtttt gatgcaccgt ggcattcggt 1167

ttccctcgat agtcatttct cagatgattt tcacccttaa taggtctgct ttagttctaa 1227

aactcggatg atttgtaatt tccagtgtcc aaatctacta attttattaa aaaaa 1282

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<223> G782

<400> 138

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 35 40 45
 Val Gln Leu Leu Lys Glu Leu Thr Ser Glu Val Asn Lys Leu Lys Ser
 50 55 60
 Glu Tyr Thr Ala Leu Thr Asp Glu Ser Arg Glu Leu Thr Gln Glu Lys
 65 70 75 80
 Asn Asp Leu Arg Glu Glu Lys Thr Ser Leu Lys Ser Asp Ile Glu Asn
 85 90 95
 Leu Asn Leu Gln Tyr Gln Gln Arg Leu Arg Ser Met Ser Pro Trp Gly
 100 105 110
 Ala Ala Met Asp His Thr Val Met Met Ala Pro Pro Pro Ser Phe Pro
 115 120 125
 Tyr Pro Met Pro Ile Ala Met Pro Pro Gly Ser Ile Pro Met His Pro
 130 135 140
 Ser Met Pro Ser Tyr Thr Tyr Phe Gly Asn Gln Asn Pro Ser Met Ile
 145 150 155 160
 Pro Ala Pro Cys Pro Thr Tyr Met Pro Tyr Met Pro Pro Asn Thr Val
 165 170 175
 Val Glu Gln Gln Ser Val His Ile Pro Gln Asn Pro Gly Asn Arg Ser
 180 185 190
 Arg Glu Pro Arg Ala Lys Val Ser Arg Glu Ser Arg Ser Glu Lys Ala
 195 200 205
 Glu Asp Ser Asn Glu Val Ala Thr Gln Leu Glu Leu Lys Thr Pro Gly
 210 215 220
 Ser Thr Ser Asp Lys Asp Thr Leu Gln Arg Pro Glu Lys Thr Lys Arg
 225 230 235 240
 Cys Lys Arg Asn Asn Asn Asn Asn Ser Ile Glu Glu Ser Ser His Ser
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 1 5 10

gaa gca aat gct act gca gat gaa aga tgt aga aaa ggt aaa gta ccg 161
 Glu Ala Asn Ala Thr Ala Asp Glu Arg Cys Arg Lys Gly Lys Val Pro
 15 20 25

aaa agg atc aac aag gcc gtt cgt gag agg ctt aag cgt gag cat ttg 209
 Lys Arg Ile Asn Lys Ala Val Arg Glu Arg Leu Lys Arg Glu His Leu
 30 35 40

aat gag ctt ttc att gaa tta gcc gat act ctt gaa ctg aat caa cag 257
 Asn Glu Leu Phe Ile Glu Leu Ala Asp Thr Leu Glu Leu Asn Gln Gln
 45 50 55

aac agt ggg aaa gct tct ata cta tgc gaa gct act cga ttc ttg aag 305
 Asn Ser Gly Lys Ala Ser Ile Leu Cys Glu Ala Thr Arg Phe Leu Lys
 60 65 70 75

gac gtg ttt ggt caa att gag tct ctt aga aag gag cat gct tct ctc 353
 Asp Val Phe Gly Gln Ile Glu Ser Leu Arg Lys Glu His Ala Ser Leu
 80 85 90

cta tct gaa tct agc tat gta acc aca gag aag aat gag ctc aag gaa 401
 Leu Ser Glu Ser Ser Tyr Val Thr Thr Glu Lys Asn Glu Leu Lys Glu
 95 100 105

gaa aca tca gtg ctt gag act gag att tcg aaa cta caa aac gag att 449
 Glu Thr Ser Val Leu Glu Thr Glu Ile Ser Lys Leu Gln Asn Glu Ile
 110 115 120

gaa gct aga gcg aat cag tcg aaa cct gac ttg aac acc tct cct gca 497
 Glu Ala Arg Ala Asn Gln Ser Lys Pro Asp Leu Asn Thr Ser Pro Ala
 125 130 135

ccc gag tac cat cat cat cat tat caa caa caa cat cct gaa cgt gta 545
 Pro Glu Tyr His His His His Tyr Gln Gln Gln His Pro Glu Arg Val
 140 145 150 155

tct cag ttc cca gga ctt ccc att ttc caa ggc ccc ggc ttt caa caa 593
 Ser Gln Phe Pro Gly Leu Pro Ile Phe Gln Gly Pro Gly Phe Gln Gln
 160 165 170

tct gct aca act ctt cat cct cct gca aca gtt ctt gtc ctt cca ata 641
 Ser Ala Thr Thr Leu His Pro Pro Ala Thr Val Leu Val Leu Pro Ile
 175 180 185

caa cct gat ccc cag aca caa gat atc tca gaa atg act caa gcg cag 689
 Gln Pro Asp Pro Gln Thr Gln Asp Ile Ser Glu Met Thr Gln Ala Gln
 190 195 200

cag cct ttg atg ttt aat agc tca aat gtg agt aac cca tgt cca agg 737
 Gln Pro Leu Met Phe Asn Ser Ser Asn Val Ser Asn Pro Cys Pro Arg
 205 210 215

tat gct agc gcg gct gac tcg tgg tct tct cgg cta ctt gga gag cgg 785
 Tyr Ala Ser Ala Ala Asp Ser Trp Ser Ser Arg Leu Leu Gly Glu Arg
 220 225 230 235

ctg aaa gcc agt gaa tgaggtcttg aacggctcca catggagtag caacgcaagt 840
 Leu Lys Ala Ser Glu
 240

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tgtccttgtg ggtttggcct tggctatttc ttgtttttga tggttgttca taggatcagg 960

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aaaaaaaaa 1027

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 35 40 45

Glu Leu Ala Asp Thr Leu Glu Leu Asn Gln Gln Asn Ser Gly Lys Ala
 50 55 60

Ser Ile Leu Cys Glu Ala Thr Arg Phe Leu Lys Asp Val Phe Gly Gln
 65 70 75 80

Ile Glu Ser Leu Arg Lys Glu His Ala Ser Leu Leu Ser Glu Ser Ser
 85 90 95

Tyr Val Thr Thr Glu Lys Asn Glu Leu Lys Glu Glu Thr Ser Val Leu
100 105 110

Glu Thr Glu Ile Ser Lys Leu Gln Asn Glu Ile Glu Ala Arg Ala Asn
115 120 125

Gln Ser Lys Pro Asp Leu Asn Thr Ser Pro Ala Pro Glu Tyr His His
130 135 140

His His Tyr Gln Gln Gln His Pro Glu Arg Val Ser Gln Phe Pro Gly
145 150 155 160

Leu Pro Ile Phe Gln Gly Pro Gly Phe Gln Gln Ser Ala Thr Thr Leu
165 170 175

His Pro Pro Ala Thr Val Leu Val Leu Pro Ile Gln Pro Asp Pro Gln
180 185 190

Thr Gln Asp Ile Ser Glu Met Thr Gln Ala Gln Gln Pro Leu Met Phe
195 200 205

Asn Ser Ser Asn Val Ser Asn Pro Cys Pro Arg Tyr Ala Ser Ala Ala
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225 230 235 240

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<223> G786

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ctacttttga tttcgaaaaa atttactgtg agttgttaaa gagtctggta ttctgaagag 180

ctgtctgtgg gggagcttct gggttggggg gtaagggtc tgggtggaaac tcgtgatatc 240

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agtaactgag cagctggaag cttacaaagg cgacaaatcg gtagtagaaa atattcaagc 360

agcttgcaagt ttgaggtgta caacttgttt ttctctttgc gtttcctttt ttacgtttgc 420

acggggttttc tg atg cag aac aat cag ttt cct cac ttc tca gat gaa gtg 471

Met Gln Asn Asn Gln Phe Pro His Phe Ser Asp Glu Val

1

5

10

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Gly Asp Arg Asn Met His Asn Pro Tyr Ala Ser Gly Ser Ser Tyr Asp	
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Ala Leu Phe Pro Pro Cys Ala Lys Leu Pro Tyr His Gly Val Glu Leu	
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caa ccg tct gcg gtc tgt cca aag aac ttt gtc atc ttc gat caa aca	615
Gln Pro Ser Ala Val Cys Pro Lys Asn Phe Val Ile Phe Asp Gln Thr	
50 55 60	
tat gac cgc agc caa gtg atg tac cat cct gag ctg act cat aag ctc	663
Tyr Asp Arg Ser Gln Val Met Tyr His Pro Glu Leu Thr His Lys Leu	
65 70 75	
atg aat acc cct tcg ttg aac aat tta gct tcg acg ttt cag aac gag	711
Met Asn Thr Pro Ser Leu Asn Asn Leu Ala Ser Thr Phe Gln Asn Glu	
80 85 90	
tat gtt ggg gga agt tat ggt aac tat ggt aac tat gag caa gaa gta	759
Tyr Val Gly Gly Ser Tyr Gly Asn Tyr Gly Asn Tyr Glu Gln Glu Val	
95 100 105	
tcc tct tct tat caa gaa gat cca aat gag atc gat gct ctc ttg agc	807
Ser Ser Ser Tyr Gln Glu Asp Pro Asn Glu Ile Asp Ala Leu Leu Ser	
110 115 120 125	
gca gat gaa gat tat gaa gag aat gat gat aat gaa ggt gaa gag gat	855
Ala Asp Glu Asp Tyr Glu Glu Asn Asp Asp Asn Glu Gly Glu Glu Asp	
130 135 140	
ggt ggt gat tca gaa gaa gtc agc act gct cgt act tct tcc agg gat	903
Gly Gly Asp Ser Glu Glu Val Ser Thr Ala Arg Thr Ser Ser Arg Asp	
145 150 155	
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Tyr Gly Asn Thr Thr Ala Glu Ser Cys Cys Ser Ser Tyr Gly Tyr Asn	
160 165 170	
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Asn Asn Asn Asn Asn Asn Ser Arg Lys Gln Ser Leu Ser Gly Ser Ala	
175 180 185	
agt agt agt aac aat gat ggg aaa gga cgt aaa aag atg aag aag atg	1047
Ser Ser Ser Asn Asn Asp Gly Lys Gly Arg Lys Lys Met Lys Lys Met	
190 195 200 205	
atg gga gta ttg agg aga att gtc cct gga gga gaa cag atg aat aca	1095
Met Gly Val Leu Arg Arg Ile Val Pro Gly Gly Glu Gln Met Asn Thr	
210 215 220	
gct tgc gtt ctt gat gaa gct gtt cag tat ctc aag tca ctt aaa atc	1143
Ala Cys Val Leu Asp Glu Ala Val Gln Tyr Leu Lys Ser Leu Lys Ile	
225 230 235	

gaa gct cag aaa ctt ggc gtt gga cat ttc tca aac caa tct 1185
 Glu Ala Gln Lys Leu Gly Val Gly His Phe Ser Asn Gln Ser
 240 245 250

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 ggcaggatgg tatctatctt atgtttgaat ctctctatgt attttgcttt ttgtgtgtta 1365
 ctgcttcgat gaagaagcaa ggtttgaaca agtacttgtg gatttgattt gagattttta 1425
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<213> Arabidopsis thaliana

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<223> G786

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 35 40 45
 Ala Val Cys Pro Lys Asn Phe Val Ile Phe Asp Gln Thr Tyr Asp Arg
 50 55 60
 Ser Gln Val Met Tyr His Pro Glu Leu Thr His Lys Leu Met Asn Thr
 65 70 75 80
 Pro Ser Leu Asn Asn Leu Ala Ser Thr Phe Gln Asn Glu Tyr Val Gly
 85 90 95
 Gly Ser Tyr Gly Asn Tyr Gly Asn Tyr Glu Gln Glu Val Ser Ser Ser
 100 105 110
 Tyr Gln Glu Asp Pro Asn Glu Ile Asp Ala Leu Leu Ser Ala Asp Glu
 115 120 125
 Asp Tyr Glu Glu Asn Asp Asp Asn Glu Gly Glu Glu Asp Gly Gly Asp
 130 135 140
 Ser Glu Glu Val Ser Thr Ala Arg Thr Ser Ser Arg Asp Tyr Gly Asn
 145 150 155 160
 Thr Thr Ala Glu Ser Cys Cys Ser Ser Tyr Gly Tyr Asn Asn Asn Asn
 165 170 175

Asn Asn Asn Ser Arg Lys Gln Ser Leu Ser Gly Ser Ala Ser Ser Ser
180 185 190

Asn Asn Asp Gly Lys Gly Arg Lys Lys Met Lys Lys Met Met Gly Val
195 200 205

Leu Arg Arg Ile Val Pro Gly Gly Glu Gln Met Asn Thr Ala Cys Val
210 215 220

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ctttactcgt ttccttc atg gct aat aac aac aac atc cca cat gat agc 170
Met Ala Asn Asn Asn Asn Ile Pro His Asp Ser
1 5 10

atc tcc gat cca tct cct acc gac gat ttc ttc gag cag atc ctc ggg 218
Ile Ser Asp Pro Ser Pro Thr Asp Asp Phe Phe Glu Gln Ile Leu Gly
15 20 25

ctt tcc aac ttc tcc ggt tct tca ggt tct ggt ctc tct gga atc ggc 266
Leu Ser Asn Phe Ser Gly Ser Ser Gly Ser Gly Leu Ser Gly Ile Gly
30 35 40

ggc gtg ggt cca cct ccg atg atg ctt cag ctt ggt tca ggc aac gaa 314
Gly Val Gly Pro Pro Pro Met Met Leu Gln Leu Gly Ser Gly Asn Glu
45 50 55

ggg aat cat aat cat atg ggt gcc att gga gga ggt gga cct gta ggg 362
Gly Asn His Asn His Met Gly Ala Ile Gly Gly Gly Gly Pro Val Gly
60 65 70 75

ttt cat aat cag atg ttt ccg ttg gga tta agt ctc gat caa ggg aaa 410
Phe His Asn Gln Met Phe Pro Leu Gly Leu Ser Leu Asp Gln Gly Lys
80 85 90

556160"51543660

gga cat ggc ttt ctt aaa cct gat gaa act ggt aaa cgt ttc caa gac 458
 Gly His Gly Phe Leu Lys Pro Asp Glu Thr Gly Lys Arg Phe Gln Asp
 95 100 105

gat gtt ctt gat aat cga tgt tcc tct atg aaa cct att ttc cat ggg 506
 Asp Val Leu Asp Asn Arg Cys Ser Ser Met Lys Pro Ile Phe His Gly
 110 115 120

cag cca atg tca cag cca gct cca cca atg ccg cat caa cag tct act 554
 Gln Pro Met Ser Gln Pro Ala Pro Pro Met Pro His Gln Gln Ser Thr
 125 130 135

att cgg cct aga gtt agg gct agg cga ggt caa gct acc gat cca cat 602
 Ile Arg Pro Arg Val Arg Ala Arg Arg Gly Gln Ala Thr Asp Pro His
 140 145 150 155

agc atc gct gag agg ctc cga agg gaa aga ata gca gaa cgg atc agg 650
 Ser Ile Ala Glu Arg Leu Arg Arg Glu Arg Ile Ala Glu Arg Ile Arg
 160 165 170

tcg ttg cag gaa ctt gta cct acc gtt aac aag aca gat agg gct gct 698
 Ser Leu Gln Glu Leu Val Pro Thr Val Asn Lys Thr Asp Arg Ala Ala
 175 180 185

atg atc gac gag att gtc gat tat gta aag ttt ctc agg ctc caa gtt 746
 Met Ile Asp Glu Ile Val Asp Tyr Val Lys Phe Leu Arg Leu Gln Val
 190 195 200

aag gtc ctg agc atg agc cgt ctt ggt gga gcc ggt gct gtc gca cca 794
 Lys Val Leu Ser Met Ser Arg Leu Gly Gly Ala Gly Ala Val Ala Pro
 205 210 215

cta gtc act gaa atg cca tta tct tca tca gtt gag gat gag acg cag 842
 Leu Val Thr Glu Met Pro Leu Ser Ser Ser Val Glu Asp Glu Thr Gln
 220 225 230 235

gcc gtg tgg gag aaa tgg tca aac gat ggg aca gag agg caa gtg gct 890
 Ala Val Trp Glu Lys Trp Ser Asn Asp Gly Thr Glu Arg Gln Val Ala
 240 245 250

aag ctg atg gaa gaa aac gtt gga gca gcg atg caa ctt ttg caa tca 938
 Lys Leu Met Glu Glu Asn Val Gly Ala Ala Met Gln Leu Leu Gln Ser
 255 260 265

aag gct ctt tgc ata atg ccg atc tca ttg gca atg gcg att tac cat 986
 Lys Ala Leu Cys Ile Met Pro Ile Ser Leu Ala Met Ala Ile Tyr His
 270 275 280

tct cag cca cca gac aca tct tct tca atc gtc aaa cca gag atg aat 1034
 Ser Gln Pro Pro Asp Thr Ser Ser Ser Ile Val Lys Pro Glu Met Asn
 285 290 295

cct cca ccg tagatcttttg ttcattccaac ggtccccagc tgatgattga 1083
 Pro Pro Pro
 300

cattttgctc tgtttccac tactagactt ttgtgactca tgaaaggtaa gtaaaaaggc 1143

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 35 40 45
 Pro Met Met Leu Gln Leu Gly Ser Gly Asn Glu Gly Asn His Asn His
 50 55 60
 Met Gly Ala Ile Gly Gly Gly Gly Pro Val Gly Phe His Asn Gln Met
 65 70 75 80
 Phe Pro Leu Gly Leu Ser Leu Asp Gln Gly Lys Gly His Gly Phe Leu
 85 90 95
 Lys Pro Asp Glu Thr Gly Lys Arg Phe Gln Asp Asp Val Leu Asp Asn
 100 105 110
 Arg Cys Ser Ser Met Lys Pro Ile Phe His Gly Gln Pro Met Ser Gln
 115 120 125
 Pro Ala Pro Pro Met Pro His Gln Gln Ser Thr Ile Arg Pro Arg Val
 130 135 140
 Arg Ala Arg Arg Gly Gln Ala Thr Asp Pro His Ser Ile Ala Glu Arg
 145 150 155 160
 Leu Arg Arg Glu Arg Ile Ala Glu Arg Ile Arg Ser Leu Gln Glu Leu
 165 170 175
 Val Pro Thr Val Asn Lys Thr Asp Arg Ala Ala Met Ile Asp Glu Ile
 180 185 190
 Val Asp Tyr Val Lys Phe Leu Arg Leu Gln Val Lys Val Leu Ser Met
 195 200 205

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Ser Arg Leu Gly Gly Ala Gly Ala Val Ala Pro Leu Val Thr Glu Met
 210 215 220

Pro Leu Ser Ser Ser Val Glu Asp Glu Thr Gln Ala Val Trp Glu Lys
 225 230 235 240

Trp Ser Asn Asp Gly Thr Glu Arg Gln Val Ala Lys Leu Met Glu Glu
 245 250 255

Asn Val Gly Ala Ala Met Gln Leu Leu Gln Ser Lys Ala Leu Cys Ile
 260 265 270

Met Pro Ile Ser Leu Ala Met Ala Ile Tyr His Ser Gln Pro Pro Asp
 275 280 285

Thr Ser Ser Ser Ile Val Lys Pro Glu Met Asn Pro Pro Pro
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 <223> G801

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 Asn Gly Ile Ile Val Glu Gln Thr Ser Asn Lys Gly Pro Leu Asn Ala
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gtt aag aaa cca ccg tct aaa gat cga cac agc aaa gtt gac gga aga 149
 Val Lys Lys Pro Pro Ser Lys Asp Arg His Ser Lys Val Asp Gly Arg
 30 35 40

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 Gly Arg Arg Ile Arg Met Pro Ile Ile Cys Ala Ala Arg Val Phe Gln
 45 50 55

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 Leu Thr Arg Glu Leu Gly His Lys Ser Asp Gly Gln Thr Ile Glu Trp
 60 65 70

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 Leu Leu Arg Gln Ala Glu Pro Ser Ile Ile Ala Ala Thr Gly Thr Gly
 75 80 85

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 Lys Ser Asp Gly Gln Thr Ile Glu Trp Leu Leu Arg Gln Ala Glu Pro
 65 70 75 80
 Ser Ile Ile Ala Ala Thr Gly Thr Gly Thr Thr Pro Ala Ser Phe Ser
 85 90 95
 Thr Ala Ser Leu Ser Thr Ser Ser Pro Phe Thr Leu Gly Lys Arg Val
 100 105 110
 Val Arg Ala Glu Glu Gly Glu Ser Gly Gly Gly Gly Gly Gly Gly Leu
 115 120 125
 Thr Val Gly His Thr Met Gly Thr Ser Leu Met Gly Gly Gly Gly Ser
 130 135 140
 Gly Gly Phe Trp Ala Val Pro Ala Arg Pro Asp Phe Gly Gln Val Trp
 145 150 155 160
 Ser Phe Ala Thr Gly Ala Pro Pro Glu Met Val Phe Ala Gln Gln Gln
 165 170 175
 Gln Pro Ala Thr Leu Phe Val Arg His Gln Gln Gln Gln Gln Ala Ser
 180 185 190
 Ala Ala Ala Ala Ala Ala Met Gly Glu Ala Ser Ala Ala Arg Val Gly
 195 200 205
 Asn Tyr Leu Pro Gly His His Leu Asn Leu Leu Ala Ser Leu Ser Gly
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Asn	Asp	Thr	Ala	Ala	Val	Ala	Thr	Gly	Gly	Gly	Ala	Arg	Gln	Leu	Val	
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gac	gca	tct	ctc	tca	atc	gtt	ccc	aga	tct	aca	cct	ccc	gaa	gac	tca	268
Asp	Ala	Ser	Leu	Ser	Ile	Val	Pro	Arg	Ser	Thr	Pro	Pro	Glu	Asp	Ser	
			30					35					40			
aca	ctc	gca	aca	acc	tca	tct	acg	gca	acg	gcg	act	aca	acg	aag	cgg	316
Thr	Leu	Ala	Thr	Thr	Ser	Ser	Thr	Ala	Thr	Ala	Thr	Thr	Thr	Lys	Arg	
		45					50					55				
tcg	act	aaa	gac	cgt	cac	acg	aaa	gtc	gac	gga	aga	gga	cgt	cgg	att	364
Ser	Thr	Lys	Asp	Arg	His	Thr	Lys	Val	Asp	Gly	Arg	Gly	Arg	Arg	Ile	
	60					65					70					
cgt	atg	ccg	gcg	cta	tgt	gca	gct	aga	gtt	ttt	cag	tta	acg	aga	gag	412
Arg	Met	Pro	Ala	Leu	Cys	Ala	Ala	Arg	Val	Phe	Gln	Leu	Thr	Arg	Glu	
	75				80					85					90	
tta	ggt	cat	aaa	tcc	gat	ggt	gaa	act	att	gaa	tgg	ctt	ctt	caa	caa	460
Leu	Gly	His	Lys	Ser	Asp	Gly	Glu	Thr	Ile	Glu	Trp	Leu	Leu	Gln	Gln	
				95					100					105		
gct	gag	cca	gct	att	gtt	gct	gct	aca	ggt	aca	gga	act	att	ccg	gcg	508
Ala	Glu	Pro	Ala	Ile	Val	Ala	Ala	Thr	Gly	Thr	Gly	Thr	Ile	Pro	Ala	
			110					115					120			
aac	ttc	tct	act	tta	agt	gtt	tcg	tta	cga	agt	agt	gga	tcg	act	ctc	556
Asn	Phe	Ser	Thr	Leu	Ser	Val	Ser	Leu	Arg	Ser	Ser	Gly	Ser	Thr	Leu	
		125					130					135				
tct	gct	ccg	ccg	tcg	aaa	tcg	gtg	ccg	ctt	tac	ggt	gct	ctt	gga	ttg	604
Ser	Ala	Pro	Pro	Ser	Lys	Ser	Val	Pro	Leu	Tyr	Gly	Ala	Leu	Gly	Leu	
	140					145					150					
act	cat	cat	cag	tat	gat	gaa	caa	gga	ggc	ggc	ggt	gtg	ttt	gct	gct	652
Thr	His	His	Gln	Tyr	Asp	Glu	Gln	Gly	Gly	Gly	Gly	Val	Phe	Ala	Ala	
	155				160					165					170	
cat	acg	tcg	ccg	ctt	tta	ggg	ttt	cat	cat	cag	ctt	caa	cac	cac	cag	700
His	Thr	Ser	Pro	Leu	Leu	Gly	Phe	His	His	Gln	Leu	Gln	His	His	Gln	
				175					180					185		
aac	cag	aat	cag	aat	caa	gat	ccg	gtg	gaa	act	att	cct	gaa	ggt	gag	748
Asn	Gln	Asn	Gln	Asn	Gln	Asp	Pro	Val	Glu	Thr	Ile	Pro	Glu	Gly	Glu	
			190					195					200			
aat	ttc	tct	agg	aaa	cgg	tat	aga	tcg	gtt	gat	ttg	tct	aaa	gaa	aac	796
Asn	Phe	Ser	Arg	Lys	Arg	Tyr	Arg	Ser	Val	Asp	Leu	Ser	Lys	Glu	Asn	
		205					210					215				

gat gat cgg aaa cag aac gag aat aaa tct ttg aaa gaa agt gaa acg 844
Asp Asp Arg Lys Gln Asn Glu Asn Lys Ser Leu Lys Glu Ser Glu Thr
220 225 230

tcg ggt cct acg gcg gcg ccg atg tgg gcg gtt gcg ccg ccg agt agg 892
Ser Gly Pro Thr Ala Ala Pro Met Trp Ala Val Ala Pro Pro Ser Arg
235 240 245 250

tct ggt gct ggg aac act ttt tgg atg ctt ccg gta ccg aca acg gcc 940
Ser Gly Ala Gly Asn Thr Phe Trp Met Leu Pro Val Pro Thr Thr Ala
255 260 265

ggt aat caa atg gag agt agt agc aac aat aac acc gcc gca ggc cac 988
Gly Asn Gln Met Glu Ser Ser Ser Asn Asn Asn Thr Ala Ala Gly His
270 275 280

cgt gct cct cct atg tgg cca ttt gtg aac tct gct gga gga gga gcg 1036
Arg Ala Pro Pro Met Trp Pro Phe Val Asn Ser Ala Gly Gly Gly Ala
285 290 295

gga ggt gga ggc gga gca gcg act cac ttt atg gcg gga acg ggg ttt 1084
Gly Gly Gly Gly Gly Ala Ala Thr His Phe Met Ala Gly Thr Gly Phe
300 305 310

agt ttt ccg atg gat cag tac aga gga agt cca ctt cag tta ggt tct 1132
Ser Phe Pro Met Asp Gln Tyr Arg Gly Ser Pro Leu Gln Leu Gly Ser
315 320 325 330

ttt tta gct cag ccg cag ccg act cag aac tta gga cta agt atg ccg 1180
Phe Leu Ala Gln Pro Gln Pro Thr Gln Asn Leu Gly Leu Ser Met Pro
335 340 345

gac tcg aat ctc ggg atg tta gcc gct ttg aac tcg gct tat tca aga 1228
Asp Ser Asn Leu Gly Met Leu Ala Ala Leu Asn Ser Ala Tyr Ser Arg
350 355 360

ggc gga aac gca aac gcg aat gcg gaa caa gcg aac aat gcg gtg gag 1276
Gly Gly Asn Ala Asn Ala Asn Ala Glu Gln Ala Asn Asn Ala Val Glu
365 370 375

cat caa gag aag cag caa cag agt gat cat gat gat gat agt aga gag 1324
His Gln Glu Lys Gln Gln Gln Ser Asp His Asp Asp Asp Ser Arg Glu
380 385 390

gag aac tca aat agc tct gag tgagtgatgt aaactaatct tgtgaaatca 1375
Glu Asn Ser Asn Ser Ser Glu
395 400

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tgagattttg tgtgttggtg tttagtagtg tttagacaag aacaatttat gtgtgaagga 1495

attgttaggt ttgggtccaa atggactctc atgggtagag aatgttttca atgtatagaa 1555

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Val	Pro	Arg	Ser	Thr	Pro	Pro	Glu	Asp	Ser	Thr	Leu	Ala	Thr	Thr	Ser	35	40	45	
Ser	Thr	Ala	Thr	Ala	Thr	Thr	Thr	Lys	Arg	Ser	Thr	Lys	Asp	Arg	His	50	55	60	
Thr	Lys	Val	Asp	Gly	Arg	Gly	Arg	Arg	Ile	Arg	Met	Pro	Ala	Leu	Cys	65	70	75	80
Ala	Ala	Arg	Val	Phe	Gln	Leu	Thr	Arg	Glu	Leu	Gly	His	Lys	Ser	Asp	85	90	95	
Gly	Glu	Thr	Ile	Glu	Trp	Leu	Leu	Gln	Gln	Ala	Glu	Pro	Ala	Ile	Val	100	105	110	
Ala	Ala	Thr	Gly	Thr	Gly	Thr	Ile	Pro	Ala	Asn	Phe	Ser	Thr	Leu	Ser	115	120	125	
Val	Ser	Leu	Arg	Ser	Ser	Gly	Ser	Thr	Leu	Ser	Ala	Pro	Pro	Ser	Lys	130	135	140	
Ser	Val	Pro	Leu	Tyr	Gly	Ala	Leu	Gly	Leu	Thr	His	His	Gln	Tyr	Asp	145	150	155	160
Glu	Gln	Gly	Gly	Gly	Gly	Val	Phe	Ala	Ala	His	Thr	Ser	Pro	Leu	Leu	165	170	175	
Gly	Phe	His	His	Gln	Leu	Gln	His	His	Gln	Asn	Gln	Asn	Gln	Asn	Gln	180	185	190	
Asp	Pro	Val	Glu	Thr	Ile	Pro	Glu	Gly	Glu	Asn	Phe	Ser	Arg	Lys	Arg	195	200	205	
Tyr	Arg	Ser	Val	Asp	Leu	Ser	Lys	Glu	Asn	Asp	Asp	Arg	Lys	Gln	Asn	210	215	220	
Glu	Asn	Lys	Ser	Leu	Lys	Glu	Ser	Glu	Thr	Ser	Gly	Pro	Thr	Ala	Ala	225	230	235	240
Pro	Met	Trp	Ala	Val	Ala	Pro	Pro	Ser	Arg	Ser	Gly	Ala	Gly	Asn	Thr	245	250	255	
Phe	Trp	Met	Leu	Pro	Val	Pro	Thr	Thr	Ala	Gly	Asn	Gln	Met	Glu	Ser	260	265	270	

Ser Ser Asn Asn Asn Thr Ala Ala Gly His Arg Ala Pro Pro Met Trp
 275 280 285

Pro Phe Val Asn Ser Ala Gly Gly Gly Ala Gly Gly Gly Gly Ala
 290 295 300

Ala Thr His Phe Met Ala Gly Thr Gly Phe Ser Phe Pro Met Asp Gln
 305 310 315 320

Tyr Arg Gly Ser Pro Leu Gln Leu Gly Ser Phe Leu Ala Gln Pro Gln
 325 330 335

Pro Thr Gln Asn Leu Gly Leu Ser Met Pro Asp Ser Asn Leu Gly Met
 340 345 350

Leu Ala Ala Leu Asn Ser Ala Tyr Ser Arg Gly Gly Asn Ala Asn Ala
 355 360 365

Asn Ala Glu Gln Ala Asn Asn Ala Val Glu His Gln Glu Lys Gln Gln
 370 375 380

Gln Ser Asp His Asp Asp Asp Ser Arg Glu Glu Asn Ser Asn Ser Ser
 385 390 395 400

Glu

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t atg gcg gag gaa cag aag ata gcg tta gaa tca gaa tct ccg gcg aag 109
 Met Ala Glu Glu Gln Lys Ile Ala Leu Glu Ser Glu Ser Pro Ala Lys
 1 5 10 15

gtt acg act cct gct cca gca gat aca ccg gct cca gct ccg gca gag 157
 Val Thr Thr Pro Ala Pro Ala Asp Thr Pro Ala Pro Ala Pro Ala Glu
 20 25 30

att ccg gct cca gct cca gct ccg act ccg gct gat gtc acg aaa gac 205
 Ile Pro Ala Pro Ala Pro Ala Pro Thr Pro Ala Asp Val Thr Lys Asp
 35 40 45

gtt gca gag gag aaa att caa aac cca cct ccg gag caa att ttc gat 253
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 Ile Pro Ala Pro Ala Pro Ala Pro Thr Pro Ala Asp Val Thr Lys Asp
 35 40 45
 Val Ala Glu Glu Lys Ile Gln Asn Pro Pro Pro Glu Gln Ile Phe Asp
 50 55 60
 Asp Ser Lys Ala Leu Thr Val Val Glu Lys Pro Val Glu Glu Pro Ala
 65 70 75 80
 Pro Ala Lys Pro Ala Ser Ala Ser Leu Asp Arg Asp Val Lys Leu Ala
 85 90 95
 Asp Leu Ser Lys Glu Lys Arg Leu Ser Phe Val Arg Ala Trp Glu Glu
 100 105 110
 Ser Glu Lys Ser Lys Ala Glu Asn Lys Ala Glu Lys Lys Ile Ala Asp
 115 120 125
 Val His Ala Trp Glu Asn Ser Lys Lys Ala Ala Val Glu Ala Gln Leu
 130 135 140
 Lys Lys Ile Glu Glu Gln Leu Glu Lys Lys Lys Ala Glu Tyr Ala Glu
 145 150 155 160
 Arg Met Lys Asn Lys Val Ala Ala Ile His Lys Glu Ala Glu Glu Arg
 165 170 175
 Arg Ala Met Ile Glu Ala Lys Arg Gly Glu Asp Val Leu Lys Ala Glu
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 Glu Thr Ala Ala Lys Tyr Arg Ala Thr Gly Ile Val Pro Lys Ala Thr
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 Cys Gly Cys Phe
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 <223> G629

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[illegible]

gtt ttc tac ttg ata tcg gga atg tgg cga act tca acc gaa aga ttc 849
 Val Phe Tyr Leu Ile Ser Gly Met Trp Arg Thr Ser Thr Glu Arg Phe
 215 220 225

ttc caa tgg att gga ggg ttt cgt cca tcc gaa ctt tta aac gtt gtg 897
 Phe Gln Trp Ile Gly Gly Phe Arg Pro Ser Glu Leu Leu Asn Val Val
 230 235 240

atg cct tat ctt caa cca tta acg gat caa caa atc ttg gaa gtg aga 945
 Met Pro Tyr Leu Gln Pro Leu Thr Asp Gln Gln Ile Leu Glu Val Arg
 245 250 255

aac ctc caa caa tca tca caa caa gca gag gat gct ctg tct caa ggg 993
 Asn Leu Gln Gln Ser Ser Gln Gln Ala Glu Asp Ala Leu Ser Gln Gly
 260 265 270 275

att gat aaa ctt caa cag agt tta gct gaa agc att gtg att gat gcg 1041
 Ile Asp Lys Leu Gln Gln Ser Leu Ala Glu Ser Ile Val Ile Asp Ala
 280 285 290

gtt atc gag tcc acg cat tat ccc act cac atg gct gca gct ata gag 1089
 Val Ile Glu Ser Thr His Tyr Pro Thr His Met Ala Ala Ala Ile Glu
 295 300 305

aat ctt caa gca tta gaa gga ttt gtg aat caa gca gat cat ctg agg 1137
 Asn Leu Gln Ala Leu Glu Gly Phe Val Asn Gln Ala Asp His Leu Arg
 310 315 320

caa caa act ttg caa caa atg gcg aag atc tta acg aca aga caa tcg 1185
 Gln Gln Thr Leu Gln Gln Met Ala Lys Ile Leu Thr Thr Arg Gln Ser
 325 330 335

gct cga ggt tta cta gct tta gga gag tat ctt cat aga ctt cgt gct 1233
 Ala Arg Gly Leu Leu Ala Leu Gly Glu Tyr Leu His Arg Leu Arg Ala
 340 345 350 355

ctt agt tct ctt tgg gca gct cgt cca caa gaa cca act taaaagagga 1282
 Leu Ser Ser Leu Trp Ala Ala Arg Pro Gln Glu Pro Thr
 360 365

acttattaaa acttttaaaaa caagaaacag cagaatcaaa agtcttgaag aagcatactc 1342

atcacaaagc ttggaaggat gtttttaaaaa agatctttgt taattaagta gagtgagatt 1402

ctcttgatta gaactttatg gtttttgctt tatgaagtat ctctccagag aagattgtaa 1462

atttgggttg aaactttgta atatattaag atccaccaaa taagtttgaa atctgagcaa 1522

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<211> 368

<212> PRT

<213> Arabidopsis thaliana

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<223> G629

<400> 152

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		20						25					30		
Lys	Ser	Asp	Ile	Asn	Asp	His	Ser	Pro	Asn	Thr	Ala	Thr	Ser	Ser	Ile
		35					40					45			
Ile	Gln	Val	Asp	Pro	Arg	Ile	Asp	Asp	His	Asn	Asn	Asn	Ile	Lys	Ile
	50					55					60				
Asn	Tyr	Asp	Ser	Ser	His	Asn	Gln	Ile	Glu	Ala	Glu	Gln	Pro	Ser	Ser
65					70					75					80
Asn	Asp	Asn	Gln	Asp	Asp	Asp	Gly	Arg	Ile	His	Asp	Lys	Met	Lys	Arg
				85					90					95	
Arg	Leu	Ala	Gln	Asn	Arg	Glu	Ala	Ala	Arg	Lys	Ser	Arg	Leu	Arg	Lys
			100					105						110	
Lys	Ala	Tyr	Val	Gln	Gln	Leu	Glu	Glu	Ser	Arg	Leu	Lys	Leu	Ser	Gln
	115						120					125			
Leu	Glu	Gln	Glu	Leu	Glu	Lys	Val	Lys	Gln	Gln	Gly	His	Leu	Gly	Pro
	130					135					140				
Ser	Gly	Ser	Ile	Asn	Thr	Gly	Ile	Ala	Ser	Phe	Glu	Met	Glu	Tyr	Ser
145					150					155					160
His	Trp	Leu	Gln	Glu	Gln	Ser	Arg	Arg	Val	Ser	Glu	Leu	Arg	Thr	Ala
			165						170					175	
Leu	Gln	Ser	His	Ile	Ser	Asp	Ile	Glu	Leu	Lys	Met	Leu	Val	Glu	Ser
			180					185					190		
Cys	Leu	Asn	His	Tyr	Ala	Asn	Leu	Phe	Arg	Met	Lys	Ser	Asp	Ala	Ala
		195					200					205			
Lys	Ala	Asp	Val	Phe	Tyr	Leu	Ile	Ser	Gly	Met	Trp	Arg	Thr	Ser	Thr
	210					215					220				
Glu	Arg	Phe	Phe	Gln	Trp	Ile	Gly	Gly	Phe	Arg	Pro	Ser	Glu	Leu	Leu
225					230					235					240
Asn	Val	Val	Met	Pro	Tyr	Leu	Gln	Pro	Leu	Thr	Asp	Gln	Gln	Ile	Leu
				245					250					255	
Glu	Val	Arg	Asn	Leu	Gln	Gln	Ser	Ser	Gln	Gln	Ala	Glu	Asp	Ala	Leu
			260					265					270		
Ser	Gln	Gly	Ile	Asp	Lys	Leu	Gln	Gln	Ser	Leu	Ala	Glu	Ser	Ile	Val
	275						280					285			
Ile	Asp	Ala	Val	Ile	Glu	Ser	Thr	His	Tyr	Pro	Thr	His	Met	Ala	Ala
	290					295					300				

Ala Ile Glu Asn Leu Gln Ala Leu Glu Gly Phe Val Asn Gln Ala Asp
305 310 315 320

His Leu Arg Gln Gln Thr Leu Gln Gln Met Ala Lys Ile Leu Thr Thr
325 330 335

Arg Gln Ser Ala Arg Gly Leu Leu Ala Leu Gly Glu Tyr Leu His Arg
340 345 350

Leu Arg Ala Leu Ser Ser Leu Trp Ala Ala Arg Pro Gln Glu Pro Thr
355 360 365

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<211> 759

<212> DNA

<213> Arabidopsis thaliana

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<221> CDS

<222> (15)..(572)

<223> G630

<400> 153

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                  1                      5                      10

atg caa caa caa gac tac ttc aac ttg aac aac tac tac aac aac tta      98
Met Gln Gln Gln Asp Tyr Phe Asn Leu Asn Asn Tyr Tyr Asn Asn Leu
   15                      20                      25

aac cct tca acc aat aac aac aac ctc aat atc ctc caa tac cct caa      146
Asn Pro Ser Thr Asn Asn Asn Asn Leu Asn Ile Leu Gln Tyr Pro Gln
   30                      35                      40

att caa gaa ctc aac cta caa tct ccg gta agc aac aac tcc aca act      194
Ile Gln Glu Leu Asn Leu Gln Ser Pro Val Ser Asn Asn Ser Thr Thr
   45                      50                      55                      60

tcc gat gac gca act gaa gaa atc ttc gtc atc aac gag agg aag caa      242
Ser Asp Asp Ala Thr Glu Glu Ile Phe Val Ile Asn Glu Arg Lys Gln
   65                      70                      75

aga cgt atg gta tct aac aga gag tca gca aga aga tca aga atg aga      290
Arg Arg Met Val Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Met Arg
   80                      85                      90

aag caa aga cac tta gat gag ctt ctc tca cag gtt gct tgg ctt cga      338
Lys Gln Arg His Leu Asp Glu Leu Leu Ser Gln Val Ala Trp Leu Arg
   95                      100                      105

agc gag aac cac cag ctt tta gat aag ctt aac caa gtc tcc gac aac      386
Ser Glu Asn His Gln Leu Leu Asp Lys Leu Asn Gln Val Ser Asp Asn
  110                      115                      120

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aat gat ctt gtt att caa gag aac tcg agt ctt aaa gaa gaa aac ttg 434
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 125 130 135 140

gag ctt cgt cag gtt atc aca tcc atg aag aag ctt gga gga ggc ata 482
 Glu Leu Arg Gln Val Ile Thr Ser Met Lys Lys Leu Gly Gly Gly Ile
 145 150 155

cat gac aaa tat tct tct ccg tcg tct atg gat gaa ttg gat caa gac 530
 His Asp Lys Tyr Ser Ser Pro Ser Ser Met Asp Glu Leu Asp Gln Asp
 160 165 170

ttt tct tct atc aca gat gat cca aga act cat cat cca tca 572
 Phe Ser Ser Ile Thr Asp Asp Pro Arg Thr His His Pro Ser
 175 180 185

tgagttgttc tgatcgagaa aaacattact tcaagtttct gcctctaatac ttatctatattt 632

tctttcttttg gtatcacttt ttaaaccgtt taactacgta ccaaagtttg ggttttatattt 692

gtttttctgt tgttttgtca gaagataatt aaatgatgga tatttgaaaa aaaaaaaaaa 752

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<212> PRT

<213> Arabidopsis thaliana

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<223> G630

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Asn Asn Asn Asn Leu Asn Ile Leu Gln Tyr Pro Gln Ile Gln Glu Leu
 35 40 45

Asn Leu Gln Ser Pro Val Ser Asn Asn Ser Thr Thr Ser Asp Asp Ala
 50 55 60

Thr Glu Glu Ile Phe Val Ile Asn Glu Arg Lys Gln Arg Arg Met Val
 65 70 75 80

Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Met Arg Lys Gln Arg His
 85 90 95

Leu Asp Glu Leu Leu Ser Gln Val Ala Trp Leu Arg Ser Glu Asn His
 100 105 110

Gln Leu Leu Asp Lys Leu Asn Gln Val Ser Asp Asn Asn Asp Leu Val
 115 120 125

Ile Gln Glu Asn Ser Ser Leu Lys Glu Glu Asn Leu Glu Leu Arg Gln
130 135 140

Val Ile Thr Ser Met Lys Lys Leu Gly Gly Gly Ile His Asp Lys Tyr
145 150 155 160

Ser Ser Pro Ser Ser Met Asp Glu Leu Asp Gln Asp Phe Ser Ser Ile
165 170 175

Thr Asp Asp Pro Arg Thr His His Pro Ser
180 185

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<211> 1060

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<222> (22)..(963)

<223> G735

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Ser Gly Asn His His Trp Ser Val Asn Gly Met Thr Ser Leu Asn Arg
15 20 25

agt gct tcc gaa tgg gca ttc aat cgt ttc ata caa gaa tcc tcc gcc 147
Ser Ala Ser Glu Trp Ala Phe Asn Arg Phe Ile Gln Glu Ser Ser Ala
30 35 40

gct gca gac gac gga gaa tct acg acg gcg tgt ggt gtt tcc gtc tcc 195
Ala Ala Asp Asp Gly Glu Ser Thr Thr Ala Cys Gly Val Ser Val Ser
45 50 55

tct cct cct aat gtt cct gta gat tca gag gaa tac aga gca ttt ctc 243
Ser Pro Pro Asn Val Pro Val Asp Ser Glu Glu Tyr Arg Ala Phe Leu
60 65 70

aag agt aaa ctt aat ctt gct tgt gct gct gtc gcc atg aaa agg gga 291
Lys Ser Lys Leu Asn Leu Ala Cys Ala Ala Val Ala Met Lys Arg Gly
75 80 85 90

act ttc atc aaa cct cag gat act tct ggt aga tct gac aat ggt gga 339
Thr Phe Ile Lys Pro Gln Asp Thr Ser Gly Arg Ser Asp Asn Gly Gly
95 100 105

gcc aat gaa tca gaa caa gcc tct ctt gct tct tcc aaa gct aca cca 387
Ala Asn Glu Ser Glu Gln Ala Ser Leu Ala Ser Ser Lys Ala Thr Pro
110 115 120

atg atg agc agt gct ata aca agt gga tct gag ctc tct ggt gat gaa 435
 Met Met Ser Ser Ala Ile Thr Ser Gly Ser Glu Leu Ser Gly Asp Glu
 125 130 135

gaa gaa gct gat ggt gaa act aat atg aac cct act aat gtt aaa cgc 483
 Glu Glu Ala Asp Gly Glu Thr Asn Met Asn Pro Thr Asn Val Lys Arg
 140 145 150

gtt aaa agg atg ctc tct aat aga gaa tca gct aga cgg tcc aga aga 531
 Val Lys Arg Met Leu Ser Asn Arg Glu Ser Ala Arg Arg Ser Arg Arg
 155 160 165 170

aga aag caa gca cac ttg agt gag cta gag aca caa gtt tca cag ctt 579
 Arg Lys Gln Ala His Leu Ser Glu Leu Glu Thr Gln Val Ser Gln Leu
 175 180 185

cgt gta gag aat tca aaa ctc atg aag ggt ctc act gat gta act caa 627
 Arg Val Glu Asn Ser Lys Leu Met Lys Gly Leu Thr Asp Val Thr Gln
 190 195 200

aca ttc aat gat gca tct gta gaa aac aga gtt tta aaa gcc aat att 675
 Thr Phe Asn Asp Ala Ser Val Glu Asn Arg Val Leu Lys Ala Asn Ile
 205 210 215

gag aca cta cga gca aag gtg aaa atg gct gaa gag aca gtg aag aga 723
 Glu Thr Leu Arg Ala Lys Val Lys Met Ala Glu Glu Thr Val Lys Arg
 220 225 230

ctc act ggc ttt aac cca atg ttc cac aat atg cct cag att gtt tca 771
 Leu Thr Gly Phe Asn Pro Met Phe His Asn Met Pro Gln Ile Val Ser
 235 240 245 250

act gtc tct ctt cct tca gag aca tca aat tct cca gac act aca agc 819
 Thr Val Ser Leu Pro Ser Glu Thr Ser Asn Ser Pro Asp Thr Thr Ser
 255 260 265

agc caa gtg act aca cca gag atc att agc tcg ggg aac aaa ggc aag 867
 Ser Gln Val Thr Thr Pro Glu Ile Ile Ser Ser Gly Asn Lys Gly Lys
 270 275 280

gcc ttg ata ggg tgc aag atg aac aga aca gct tcg atg cgt agt gtt 915
 Ala Leu Ile Gly Cys Lys Met Asn Arg Thr Ala Ser Met Arg Ser Val
 285 290 295

gag agc ttg gaa cat ctg cag aaa cgt att cga agc gtt ggg gat cag 963
 Glu Ser Leu Glu His Leu Gln Lys Arg Ile Arg Ser Val Gly Asp Gln
 300 305 310

tagctgttaa agaagaatct tgatttgtaa cattaatctt aagacatatg ttaaagacaa 1023

aatgttgat gtttttggcg gccgcgaatt cctgcag 1060

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<211> 314

<212> PRT

<213> Arabidopsis thaliana

<223> G735

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Ser Val Asn Gly Met Thr Ser Leu Asn Arg Ser Ala Ser Glu Trp Ala
20 25 30

Phe Asn Arg Phe Ile Gln Glu Ser Ser Ala Ala Ala Asp Asp Gly Glu
35 40 45

Ser Thr Thr Ala Cys Gly Val Ser Val Ser Ser Pro Pro Asn Val Pro
50 55 60

Val	Asp	Ser	Glu	Glu	Tyr	Arg	Ala	Phe	Leu	Lys	Ser	Lys	Leu	Asn	Leu
65					70					75					80

Ala Cys Ala Ala Val Ala Met Lys Arg Gly Thr Phe Ile Lys Pro Gln
85 90 95

Asp Thr Ser Gly Arg Ser Asp Asn Gly Gly Ala Asn Glu Ser Glu Gln
100 105 110

Ala Ser Leu Ala Ser Ser Lys Ala Thr Pro Met Met Ser Ser Ala Ile
115 120 125

Thr Ser Gly Ser Glu Leu Ser Gly Asp Glu Glu Glu Ala Asp Gly Glu
130 135 140

Thr	Asn	Met	Asn	Pro	Thr	Asn	Val	Lys	Arg	Val	Lys	Arg	Met	Leu	Ser
145					150					155					160

Asn Arg Glu Ser Ala Arg Arg Ser Arg Arg Arg Lys Gln Ala His Leu
165 170 175

Ser Glu Leu Glu Thr Gln Val Ser Gln Leu Arg Val Glu Asn Ser Lys
180 185 190

Leu Met Lys Gly Leu Thr Asp Val Thr Gln Thr Phe Asn Asp Ala Ser
195 200 205

Val Glu Asn Arg Val Leu Lys Ala Asn Ile Glu Thr Leu Arg Ala Lys
210 215 220

Val Lys Met Ala Glu Glu Thr Val Lys Arg Leu Thr Gly Phe Asn Pro
225 230 235 240

Met Phe His Asn Met Pro Gln Ile Val Ser Thr Val Ser Leu Pro Ser
245 250 255

Glu Thr Ser Asn Ser Pro Asp Thr Thr Ser Ser Gln Val Thr Thr Pro
260 265 270

Glu Ile Ile Ser Ser Gly Asn Lys Gly Lys Ala Leu Ile Gly Cys Lys
275 280 285

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ttgcatatta	atttctttca	ttttaatacc	tgatacaaaa	aagtcgctct	aatatataat	180										
ttattctcaa	acttttcaata	cactccacac	agc	atg	gaa	act	gta	cga	tat	cca	234					
				Met	Glu	Thr	Val	Arg	Tyr	Pro						
				1					5							
aag	tac	gaa	aat	tcg	ccg	gcc	gag	acc	atg	gtg	gaa	agc	ttc	gtg	tcg	282
Lys	Tyr	Glu	Asn	Ser	Pro	Ala	Glu	Thr	Met	Val	Glu	Ser	Phe	Val	Ser	
		10				15					20					
aca	cct	tct	tca	ttt	cat	aac	cct	cca	ctt	ttc	gac	aac	aac	tta	aac	330
Thr	Pro	Ser	Ser	Phe	His	Asn	Pro	Pro	Leu	Phe	Asp	Asn	Asn	Leu	Asn	
	25					30					35					
cct	gta	gat	ggg	ttt	toc	cca	caa	tca	ttt	gac	cgt	gac	tac	aat	ttc	378
Pro	Val	Asp	Gly	Phe	Ser	Pro	Gln	Ser	Phe	Asp	Arg	Asp	Tyr	Asn	Phe	
40					45					50					55	
aac	ggc	agt	tta	tca	ggg	ctg	aac	ctt	ccc	gag	aaa	aaa	ccc	atc	aaa	426
Asn	Gly	Ser	Leu	Ser	Gly	Leu	Asn	Leu	Pro	Glu	Lys	Lys	Pro	Ile	Lys	
			60					65						70		
aag	cgc	aag	tct	tgg	gga	cag	caa	ctt	ccc	gaa	ccc	aaa	aca	aac	ctt	474
Lys	Arg	Lys	Ser	Trp	Gly	Gln	Gln	Leu	Pro	Glu	Pro	Lys	Thr	Asn	Leu	
			75					80					85			
cct	ccg	agg	aag	cgc	gca	aag	act	caa	gat	gaa	aaa	gag	caa	cgg	cgt	522
Pro	Pro	Arg	Lys	Arg	Ala	Lys	Thr	Gln	Asp	Glu	Lys	Glu	Gln	Arg	Arg	
		90					95					100				
gtt	gag	cgc	gtc	cta	cgc	aat	cgt	aga	gcg	gcc	caa	tca	tca	cga	gaa	570
Val	Glu	Arg	Val	Leu	Arg	Asn	Arg	Arg	Ala	Ala	Gln	Ser	Ser	Arg	Glu	
	105					110					115					

cga aaa cgc cag gag gtc gag gct ttg gaa gtc gag aaa cga gct att	618
Arg Lys Arg Gln Glu Val Glu Ala Leu Glu Val Glu Lys Arg Ala Ile	
120 125 130 135	
gag cgc aaa aac atg gat ctt gag atg cgc tta gca gac atg gaa gca	666
Glu Arg Lys Asn Met Asp Leu Glu Met Arg Leu Ala Asp Met Glu Ala	
140 145 150	
aag tac tac ctt ctt caa cag gaa ctg aaa cga gcc agt ggt tac aac	714
Lys Tyr Tyr Leu Leu Gln Gln Glu Leu Lys Arg Ala Ser Gly Tyr Asn	
155 160 165	
aag aca aac ttt ctt tcc tac tct gat tct tca act cca gac atc tcc	762
Lys Thr Asn Phe Leu Ser Tyr Ser Asp Ser Ser Thr Pro Asp Ile Ser	
170 175 180	
gaa gat tca caa tta tca cct ttg act ttc tct aag caa ctc ttc aac	810
Glu Asp Ser Gln Leu Ser Pro Leu Thr Phe Ser Lys Gln Leu Phe Asn	
185 190 195	
gct caa gat gaa ttg tgt cga cca ata agt cct cag tca atc ggt ccg	858
Ala Gln Asp Glu Leu Cys Arg Pro Ile Ser Pro Gln Ser Ile Gly Pro	
200 205 210 215	
ctg act tca aga acc gtt gac cct tct aca ctc tca cct aag tct tta	906
Leu Thr Ser Arg Thr Val Asp Pro Ser Thr Leu Ser Pro Lys Ser Leu	
220 225 230	
tct tct ccc gat tca tcc aat tct aat tct tcc gac atg aca caa cat	954
Ser Ser Pro Asp Ser Ser Asn Ser Asn Ser Ser Asp Met Thr Gln His	
235 240 245	
cct gcc gtg gtg ttg tgc gac ctg cag tgt cag tcg gaa ctg ggt cag	1002
Pro Ala Val Val Leu Cys Asp Leu Gln Cys Gln Ser Glu Leu Gly Gln	
250 255 260	
cct tgg atg aat tcg aca tat ctt tct ttg aga acg aaa gct ctg aaa	1050
Pro Trp Met Asn Ser Thr Tyr Leu Ser Leu Arg Thr Lys Ala Leu Lys	
265 270 275	
tta tcg gta act tac ctt att aca atg tta aca act ttt ttg att gtc	1098
Leu Ser Val Thr Tyr Leu Ile Thr Met Leu Thr Thr Phe Leu Ile Val	
280 285 290 295	
ctc gga aac ctg aat cag aat atc atg ttt tta atg acg aga ttt ctc	1146
Leu Gly Asn Leu Asn Gln Asn Ile Met Phe Leu Met Thr Arg Phe Leu	
300 305 310	
ctc aca cca acg tat ttt att cag agg atg aaa ata ttc ggg gac aga	1194
Leu Thr Pro Thr Tyr Phe Ile Gln Arg Met Lys Ile Phe Gly Asp Arg	
315 320 325	
acg acg gtg ttt tcg atg aat ttg tcg tat gtg atc ttc tca acg atg	1242
Thr Thr Val Phe Ser Met Asn Leu Ser Tyr Val Ile Phe Ser Thr Met	
330 335 340	

cga caa gcc tgc agc cgc aat ttg gcg cgt tct cta atg aat gcg acg 1338
Arg Gln Ala Cys Ser Arg Asn Leu Ala Arg Ser Leu Met Asn Ala Thr
360 365 370 375

atg gcg gca ttg cgg ttt gag tcc aaa cag cga ctt ttt cgc aat ttt 1386
Met Ala Ala Leu Arg Phe Glu Ser Lys Gln Arg Leu Phe Arg Asn Phe
380 385 390

ctc tct act gta gcg ctt cag att tct cga aga tcc tcc cac ttt tta 1434
Leu Ser Thr Val Ala Leu Gln Ile Ser Arg Arg Ser Ser His Phe Leu
395 400 405

tgg tac tgaaaatact cgaagacact aaactgaacg agagaaatga gaagcgatgg 1490
Trp Tyr

ttccaatttc aaatgtcgac cttacttat tgtgttcgat tgaggattag taaaaatcta 1550

atggtatatt tagaataata ttcataaaga aaatTTataa taaatctact caatacattg 1610

aaaaattagc ttttggattt ttactgctta ggatatagaa atggtcacag ttcatagctg 1670

ggtatagaca acgatcatga aatttttaa at gtatctatcc tccagtaagg tagtaatcaa 1730

cgattttgat cgtctaccac caaaaaaaaaa aaaaaaaaaa a 1771

<211> 409

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1034

<400> 158

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Met Val Glu Ser Phe Val Ser Thr Pro Ser Ser Phe His Asn Pro Pro
20 25 30

Leu Phe Asp Asn Asn Leu Asn Pro Val Asp Gly Phe Ser Pro Gln Ser
35 40 45

Phe Asp Arg Asp Tyr Asn Phe Asn Gly Ser Leu Ser Gly Leu Asn Leu
50 55 60

Pro Glu Lys Lys Pro Ile Lys Lys Arg Lys Ser Trp Gly Gln Gln Leu
65 70 75 80

Pro Glu Pro Lys Thr Asn Leu Pro Pro Arg Lys Arg Ala Lys Thr Gln
85 90 95

Asp	Glu	Lys	Glu	Gln	Arg	Arg	Val	Glu	Arg	Val	Leu	Arg	Asn	Arg	Arg	
			100					105					110			
Ala	Ala	Gln	Ser	Ser	Arg	Glu	Arg	Lys	Arg	Gln	Glu	Val	Glu	Ala	Leu	
		115					120					125				
Glu	Val	Glu	Lys	Arg	Ala	Ile	Glu	Arg	Lys	Asn	Met	Asp	Leu	Glu	Met	
	130					135					140					
Arg	Leu	Ala	Asp	Met	Glu	Ala	Lys	Tyr	Tyr	Leu	Leu	Gln	Gln	Glu	Leu	
145					150					155					160	
Lys	Arg	Ala	Ser	Gly	Tyr	Asn	Lys	Thr	Asn	Phe	Leu	Ser	Tyr	Ser	Asp	
				165					170					175		
Ser	Ser	Thr	Pro	Asp	Ile	Ser	Glu	Asp	Ser	Gln	Leu	Ser	Pro	Leu	Thr	
			180					185					190			
Phe	Ser	Lys	Gln	Leu	Phe	Asn	Ala	Gln	Asp	Glu	Leu	Cys	Arg	Pro	Ile	
		195					200					205				
Ser	Pro	Gln	Ser	Ile	Gly	Pro	Leu	Thr	Ser	Arg	Thr	Val	Asp	Pro	Ser	
	210					215					220					
Thr	Leu	Ser	Pro	Lys	Ser	Leu	Ser	Ser	Pro	Asp	Ser	Ser	Asn	Ser	Asn	
225				230						235					240	
Ser	Ser	Asp	Met	Thr	Gln	His	Pro	Ala	Val	Val	Leu	Cys	Asp	Leu	Gln	
				245					250					255		
Cys	Gln	Ser	Glu	Leu	Gly	Gln	Pro	Trp	Met	Asn	Ser	Thr	Tyr	Leu	Ser	
			260					265					270			
Leu	Arg	Thr	Lys	Ala	Leu	Lys	Leu	Ser	Val	Thr	Tyr	Leu	Ile	Thr	Met	
		275					280					285				
Leu	Thr	Thr	Phe	Leu	Ile	Val	Leu	Gly	Asn	Leu	Asn	Gln	Asn	Ile	Met	
	290					295					300					
Phe	Leu	Met	Thr	Arg	Phe	Leu	Leu	Thr	Pro	Thr	Tyr	Phe	Ile	Gln	Arg	
305					310					315					320	
Met	Lys	Ile	Phe	Gly	Asp	Arg	Thr	Thr	Val	Phe	Ser	Met	Asn	Leu	Ser	
				325					330					335		
Tyr	Val	Ile	Phe	Ser	Thr	Met	Lys	Leu	Tyr	Gln	Thr	Arg	Val	Cys	Ile	
			340					345					350			
Arg	Ile	Ser	Leu	Leu	Gly	Arg	Arg	Gln	Ala	Cys	Ser	Arg	Asn	Leu	Ala	
		355					360					365				
Arg	Ser	Leu	Met	Asn	Ala	Thr	Met	Ala	Ala	Leu	Arg	Phe	Glu	Ser	Lys	
	370					375					380					
Gln	Arg	Leu	Phe	Arg	Asn	Phe	Leu	Ser	Thr	Val	Ala	Leu	Gln	Ile	Ser	
385					390						395				400	

<400> 159															60
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gcgtcttaat catagtactt aattttctct gtgtgtttta at atg aat aat aaa															114
Met Asn Asn Lys															
1															
act gaa atg gga tct tcc aca agt gga aat tgc tcg tcg gtt tca acc	162														
Thr Glu Met Gly Ser Ser Thr Ser Gly Asn Cys Ser Ser Val Ser Thr															
5 10 15 20															
act ggt tta gct aac tcc ggt tca gaa tct gat ctc cgg caa cgt gat	210														
Thr Gly Leu Ala Asn Ser Gly Ser Glu Ser Asp Leu Arg Gln Arg Asp															
25 30 35															
cta atc gac gag cgg aag aga aag agg aaa cag tcg aac aga gaa tct	258														
Leu Ile Asp Glu Arg Lys Arg Lys Arg Lys Gln Ser Asn Arg Glu Ser															
40 45 50															
gcg agg agg tcg agg atg agg aag cag aag cat ttg gat gat ctc act	306														
Ala Arg Arg Ser Arg Met Arg Lys Gln Lys His Leu Asp Asp Leu Thr															
55 60 65															
gct cag gtg act cat cta cgt aaa gaa aac gct cag atc gtc gcc gga	354														
Ala Gln Val Thr His Leu Arg Lys Glu Asn Ala Gln Ile Val Ala Gly															
70 75 80															
atc gcc gtc acg acg cag cac tac gtc act atc gag gcg gag aac gac	402														
Ile Ala Val Thr Thr Gln His Tyr Val Thr Ile Glu Ala Glu Asn Asp															
85 90 95 100															
att ctc aga gct cag gtt ctt gaa ctt aac cac cgt ctc caa tct ctt	450														
Ile Leu Arg Ala Gln Val Leu Glu Leu Asn His Arg Leu Gln Ser Leu															
105 110 115															
aac gag atc gtt gat ttc gtc gaa tct tct tct tca gga ttc ggt atg	498														
Asn Glu Ile Val Asp Phe Val Glu Ser Ser Ser Ser Gly Phe Gly Met															
120 125 130															
gag acc ggt cag gga tta ttc gac ggt gga tta ttc gac ggc gtg atg	546														
Glu Thr Gly Gln Gly Leu Phe Asp Gly Gly Leu Phe Asp Gly Val Met															
135 140 145															

aat cct atg aat cta ggg ttt tat aat caa cca atc atg gct tct gct 594
 Asn Pro Met Asn Leu Gly Phe Tyr Asn Gln Pro Ile Met Ala Ser Ala
 150 155 160

tct act gct ggt gat gtt ttc aac tgt tagaaaactt cacatcatta 641
 Ser Thr Ala Gly Asp Val Phe Asn Cys
 165 170

tcacgtgag tgagactaat catcgcagca ggggtaaaac tgtaattttt cttataaatt 701
 atgtgatgat gctttgtttc tttattttat aagatgggta attagtgttt aaaactgatt 761
 gtaatgatag acagtgtaag aaatgtgtga tatcatggag atgggtgatgt gagtttggtgta 821
 caaatatttt aagatctttt ctttctatat attaaaagtg aagaaataat attttgtcat 881
 tttcttaaaa aaaaaaaaaa aa 903

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<211> 173

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1035

<400> 160

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Ser Val Ser Thr Thr Gly Leu Ala Asn Ser Gly Ser Glu Ser Asp Leu
 20 25 30

Arg Gln Arg Asp Leu Ile Asp Glu Arg Lys Arg Lys Arg Lys Gln Ser
 35 40 45

Asn Arg Glu Ser Ala Arg Arg Ser Arg Met Arg Lys Gln Lys His Leu
 50 55 60

Asp Asp Leu Thr Ala Gln Val Thr His Leu Arg Lys Glu Asn Ala Gln
 65 70 75 80

Ile Val Ala Gly Ile Ala Val Thr Thr Gln His Tyr Val Thr Ile Glu
 85 90 95

Ala Glu Asn Asp Ile Leu Arg Ala Gln Val Leu Glu Leu Asn His Arg
 100 105 110

Leu Gln Ser Leu Asn Glu Ile Val Asp Phe Val Glu Ser Ser Ser Ser
 115 120 125

Gly Phe Gly Met Glu Thr Gly Gln Gly Leu Phe Asp Gly Gly Leu Phe
 130 135 140

Asp Gly Val Met Asn Pro Met Asn Leu Gly Phe Tyr Asn Gln Pro Ile
 145 150 155 160

Met Ala Ser Ala Ser Thr Ala Gly Asp Val Phe Asn Cys
 165 170

<210> 161
 <211> 1035
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (5)..(889)
 <223> G1048

<400> 161
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 1 5 10 15

ttc ttc ttc gat ttc gat cct tca atc gta att gat tct ctt ccg gcg 97
 Phe Phe Phe Asp Phe Asp Pro Ser Ile Val Ile Asp Ser Leu Pro Ala
 20 25 30

gag gat ttt ctt cag tct tca ccg gat tca tgg atc gga gaa atc gag 145
 Glu Asp Phe Leu Gln Ser Ser Pro Asp Ser Trp Ile Gly Glu Ile Glu
 35 40 45

aat caa ttg atg aac gat gag aat cat caa gag gag agt ttt gtg gaa 193
 Asn Gln Leu Met Asn Asp Glu Asn His Gln Glu Glu Ser Phe Val Glu
 50 55 60

ttg gat cag caa tcg gtt tca gat ttc ata gcg gat cta ctc gtt gat 241
 Leu Asp Gln Gln Ser Val Ser Asp Phe Ile Ala Asp Leu Leu Val Asp
 65 70 75

tat oca act agc gat tct ggc tcc gtt gat ttg gcg gct gat aaa gtt 289
 Tyr Pro Thr Ser Asp Ser Gly Ser Val Asp Leu Ala Ala Asp Lys Val
 80 85 90 95

cta acc gtc gat tct ccc gcc gcc gct gat gat tcc ggg aag gag aat 337
 Leu Thr Val Asp Ser Pro Ala Ala Ala Asp Asp Ser Gly Lys Glu Asn
 100 105 110

tcg gat ttg gtt gtt gag aag aag tct aat gat tct ggt agc gag att 385
 Ser Asp Leu Val Val Glu Lys Lys Ser Asn Asp Ser Gly Ser Glu Ile
 115 120 125

cat gat gat gat gac gaa gaa gga gac gat gat gct gtg gct aaa aaa 433
 His Asp Asp Asp Asp Glu Glu Gly Asp Asp Asp Ala Val Ala Lys Lys
 130 135 140

cga aga agg aga gta aga aat aga gat gcg gcg gtt aga tcg aga gag 481
 Arg Arg Arg Arg Val Arg Asn Arg Asp Ala Ala Val Arg Ser Arg Glu
 145 150 155

agg aag aag gaa tat gta caa gat tta gag aag aag agt aag tat ctc 529
 Arg Lys Lys Glu Tyr Val Gln Asp Leu Glu Lys Lys Ser Lys Tyr Leu
 160 165 170 175

gaa aga gaa tgc ttg aga cta gga cgt atg ctt gag tgc ttc gtt gct 577
 Glu Arg Glu Cys Leu Arg Leu Gly Arg Met Leu Glu Cys Phe Val Ala
 180 185 190

gaa aac cag tct cta cgt tac tgt ttg caa aag ggt aat ggc aat aat 625
 Glu Asn Gln Ser Leu Arg Tyr Cys Leu Gln Lys Gly Asn Gly Asn Asn
 195 200 205

act acc atg atg tcg aag cag gag tct gct gtg ctc ttg ttg gaa tcc 673
 Thr Thr Met Met Ser Lys Gln Glu Ser Ala Val Leu Leu Leu Glu Ser
 210 215 220

ctg ctg ttg ggt tcc ctg ctt tgg ctt ctg gga gta aac ttc att tgc 721
 Leu Leu Leu Gly Ser Leu Leu Trp Leu Leu Gly Val Asn Phe Ile Cys
 225 230 235

cta ttc cct tat atg tcc cac aca aag tgt tgc ctc cta cgt cca gaa 769
 Leu Phe Pro Tyr Met Ser His Thr Lys Cys Cys Leu Leu Arg Pro Glu
 240 245 250 255

cca gaa aag ctg gtt cta aac ggg ctc ggg agt agt agc aaa ccg tct 817
 Pro Glu Lys Leu Val Leu Asn Gly Leu Gly Ser Ser Ser Lys Pro Ser
 260 265 270

tat acc ggc gtt agt cgg aga tgt aag ggt tcg agg cct agg atg aaa 865
 Tyr Thr Gly Val Ser Arg Arg Cys Lys Gly Ser Arg Pro Arg Met Lys
 275 280 285

tac caa atc tta acc ctt gcg gcg tgacaacgcc ttttttaact gcttcttttg 919
 Tyr Gln Ile Leu Thr Leu Ala Ala
 290 295

cgcattttga gttgtagatg agtgtctttt agttttctct ctcttggttt gtatttcgct 979

gttgaaagtt ttctgtctaa tatcgataag ttaacagtga aaaaaaaaaa aaaaaa 1035

<210> 162

<211> 295

<212> PRT

<213> Arabidopsis thaliana

<220>

<223> G1048

<400> 162

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Phe Phe Asp Phe Asp Pro Ser Ile Val Ile Asp Ser Leu Pro Ala Glu
 20 25 30

Asp Phe Leu Gln Ser Ser Pro Asp Ser Trp Ile Gly Glu Ile Glu Asn
 35 40 45

Gln Leu Met Asn Asp Glu Asn His Gln Glu Glu Ser Phe Val Glu Leu
 50 55 60

Asp Gln Gln Ser Val Ser Asp Phe Ile Ala Asp Leu Leu Val Asp Tyr
 65 70 75 80
 Pro Thr Ser Asp Ser Gly Ser Val Asp Leu Ala Ala Asp Lys Val Leu
 85 90 95
 Thr Val Asp Ser Pro Ala Ala Ala Asp Asp Ser Gly Lys Glu Asn Ser
 100 105 110
 Asp Leu Val Val Glu Lys Lys Ser Asn Asp Ser Gly Ser Glu Ile His
 115 120 125
 Asp Asp Asp Asp Glu Glu Gly Asp Asp Asp Ala Val Ala Lys Lys Arg
 130 135 140
 Arg Arg Arg Val Arg Asn Arg Asp Ala Ala Val Arg Ser Arg Glu Arg
 145 150 155 160
 Lys Lys Glu Tyr Val Gln Asp Leu Glu Lys Lys Ser Lys Tyr Leu Glu
 165 170 175
 Arg Glu Cys Leu Arg Leu Gly Arg Met Leu Glu Cys Phe Val Ala Glu
 180 185 190
 Asn Gln Ser Leu Arg Tyr Cys Leu Gln Lys Gly Asn Gly Asn Asn Thr
 195 200 205
 Thr Met Met Ser Lys Gln Glu Ser Ala Val Leu Leu Leu Glu Ser Leu
 210 215 220
 Leu Leu Gly Ser Leu Leu Trp Leu Leu Gly Val Asn Phe Ile Cys Leu
 225 230 235 240
 Phe Pro Tyr Met Ser His Thr Lys Cys Cys Leu Leu Arg Pro Glu Pro
 245 250 255
 Glu Lys Leu Val Leu Asn Gly Leu Gly Ser Ser Ser Lys Pro Ser Tyr
 260 265 270
 Thr Gly Val Ser Arg Arg Cys Lys Gly Ser Arg Pro Arg Met Lys Tyr
 275 280 285
 Gln Ile Leu Thr Leu Ala Ala
 290 295

<210> 163

<211> 1421

<212> DNA

<213> Arabidopsis thaliana

<220>

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<222> (17) .. (1126)

<223> G1058

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gct gag gaa gct cag gcc atg gcc atg act tct gcg cca gct gct aca 100
 Ala Glu Glu Ala Gln Ala Met Ala Met Thr Ser Ala Pro Ala Ala Thr
 15 20 25

gcg gta gcg caa cct ggt gct ggt atc cca ccc cca ggt ggg aat ctc 148
 Ala Val Ala Gln Pro Gly Ala Gly Ile Pro Pro Pro Gly Gly Asn Leu
 30 35 40

cag agg caa ggt tcg ttg acg ttg cct aga aca att agt cag aag act 196
 Gln Arg Gln Gly Ser Leu Thr Leu Pro Arg Thr Ile Ser Gln Lys Thr
 45 50 55 60

gtt gat gag gtg tgg aaa tgt ttg atc acc aag gat ggt aat atg gaa 244
 Val Asp Glu Val Trp Lys Cys Leu Ile Thr Lys Asp Gly Asn Met Glu
 65 70 75

ggt agc agc gga ggc ggt ggt gag tcg aat gtg cct cct gga agg caa 292
 Gly Ser Ser Gly Gly Gly Gly Glu Ser Asn Val Pro Pro Gly Arg Gln
 80 85 90

cag act tta ggg gaa atg aca ctt gaa gaa ttt ctg ttc cgt gct ggg 340
 Gln Thr Leu Gly Glu Met Thr Leu Glu Glu Phe Leu Phe Arg Ala Gly
 95 100 105

gtt gta aga gaa gat aac tgt gtt caa cag atg ggt cag gtc aac gga 388
 Val Val Arg Glu Asp Asn Cys Val Gln Gln Met Gly Gln Val Asn Gly
 110 115 120

aac aat aac aat ggg ttt tat ggt aac agc act gct gct ggc ggc tta 436
 Asn Asn Asn Asn Gly Phe Tyr Gly Asn Ser Thr Ala Ala Gly Gly Leu
 125 130 135 140

ggt ttt gga ttt ggt cag cca aat caa aac agc ata aca ttc aat ggt 484
 Gly Phe Gly Phe Gly Gln Pro Asn Gln Asn Ser Ile Thr Phe Asn Gly
 145 150 155

act aat gat tct atg atc ttg aat cag cca cct ggt tta ggg ctc aaa 532
 Thr Asn Asp Ser Met Ile Leu Asn Gln Pro Pro Gly Leu Gly Leu Lys
 160 165 170

atg ggt gga aca atg cag cag caa caa caa caa cag cag ttg ctt cag 580
 Met Gly Gly Thr Met Gln Gln Gln Gln Gln Gln Gln Gln Leu Leu Gln
 175 180 185

cag caa caa cag cag atg cag cag ctg aat cag cct cat cca cag cag 628
 Gln Gln Gln Gln Gln Met Gln Gln Leu Asn Gln Pro His Pro Gln Gln
 190 195 200

cgg ctg cct caa acc att ttt cct aaa caa gca aac gta gca ttt tct 676
 Arg Leu Pro Gln Thr Ile Phe Pro Lys Gln Ala Asn Val Ala Phe Ser
 205 210 215 220

gcg cct gtg aat ata acc aac aag ggt ttt gct ggg gct gca aat aat 724
Ala Pro Val Asn Ile Thr Asn Lys Gly Phe Ala Gly Ala Ala Asn Asn
225 230 235

tct atc aac aat aat aat gga tta gct agt tac gga gga acc ggg gtc 772
Ser Ile Asn Asn Asn Asn Gly Leu Ala Ser Tyr Gly Gly Thr Gly Val
240 245 250

act gtt gca gca act tct cca gga aca agc agc gca gaa aat aat tct 820
Thr Val Ala Ala Thr Ser Pro Gly Thr Ser Ser Ala Glu Asn Asn Ser
255 260 265

tta tca cca gtt ccg tat gtg ctt aat cga gga cga aga agc aat aca 868
Leu Ser Pro Val Pro Tyr Val Leu Asn Arg Gly Arg Arg Ser Asn Thr
270 275 280

ggt cta gag aag gtt atc gag agg agg caa agg aga atg atc aag aat 916
Gly Leu Glu Lys Val Ile Glu Arg Arg Gln Arg Arg Met Ile Lys Asn
285 290 295 300

cgg gaa tca gct gct aga tca aga gct cga aag cag gct tat aca ttg 964
Arg Glu Ser Ala Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Leu
305 310 315

gaa ctg gaa gcc gaa att gaa aag ctc aag aaa acg aat caa gaa ctg 1012
Glu Leu Glu Ala Glu Ile Glu Lys Leu Lys Lys Thr Asn Gln Glu Leu
320 325 330

cag aaa aaa cag gct gaa atg gtg gaa atg cag aag aat gag ctg aaa 1060
Gln Lys Lys Gln Ala Glu Met Val Glu Met Gln Lys Asn Glu Leu Lys
335 340 345

gaa acg tcg aag cga ccg tgg ggc agc aaa agg caa tgc ttg aga agg 1108
Glu Thr Ser Lys Arg Pro Trp Gly Ser Lys Arg Gln Cys Leu Arg Arg
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aca tta acc gga cca tgg tgaaggatga agcaacaaga acggatgaac 1156
Thr Leu Thr Gly Pro Trp
365 370

cagactccta gcttgggatt aatgtaatag gatagtgcta cctgtacagg agattaagag 1216

aaattgagtg aaagatctag gttacagagt aggagagagt tttcattatg aataaatgac 1276

attttgtgcc ctgacctttg ttagtttagg tttagattat cctctgttat tgacttattg 1336

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 35 40 45
 Ser Leu Thr Leu Pro Arg Thr Ile Ser Gln Lys Thr Val Asp Glu Val
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 Trp Lys Cys Leu Ile Thr Lys Asp Gly Asn Met Glu Gly Ser Ser Gly
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 Gly Gly Gly Glu Ser Asn Val Pro Pro Gly Arg Gln Gln Thr Leu Gly
 85 90 95
 Glu Met Thr Leu Glu Glu Phe Leu Phe Arg Ala Gly Val Val Arg Glu
 100 105 110
 Asp Asn Cys Val Gln Gln Met Gly Gln Val Asn Gly Asn Asn Asn Asn
 115 120 125
 Gly Phe Tyr Gly Asn Ser Thr Ala Ala Gly Gly Leu Gly Phe Gly Phe
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 Gly Gln Pro Asn Gln Asn Ser Ile Thr Phe Asn Gly Thr Asn Asp Ser
 145 150 155 160
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 Gln Met Gln Gln Leu Asn Gln Pro His Pro Gln Gln Arg Leu Pro Gln
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 210 215 220
 Ile Thr Asn Lys Gly Phe Ala Gly Ala Ala Asn Asn Ser Ile Asn Asn
 225 230 235 240
 Asn Asn Gly Leu Ala Ser Tyr Gly Gly Thr Gly Val Thr Val Ala Ala
 245 250 255
 Thr Ser Pro Gly Thr Ser Ser Ala Glu Asn Asn Ser Leu Ser Pro Val
 260 265 270
 Pro Tyr Val Leu Asn Arg Gly Arg Arg Ser Asn Thr Gly Leu Glu Lys
 275 280 285
 Val Ile Glu Arg Arg Gln Arg Arg Met Ile Lys Asn Arg Glu Ser Ala
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Ala Arg Ser Arg Ala Arg Lys Gln Ala Tyr Thr Leu Glu Leu Glu Ala
305 310 315 320

Glu Ile Glu Lys Leu Lys Lys Thr Asn Gln Glu Leu Gln Lys Lys Gln
325 330 335

Ala Glu Met Val Glu Met Gln Lys Asn Glu Leu Lys Glu Thr Ser Lys
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Arg Pro Trp Gly Ser Lys Arg Gln Cys Leu Arg Arg Thr Leu Thr Gly
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Pro Trp
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acaaatcggg tatgggggaa tttgggtttt aagatagcgt gatctgtaat aataagtgg 180

tcgcgatcgt gatcaagaaa ctgggtggctg atagtgatat gcatatttga gag atg 236
Met
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Val Phe Lys Arg Lys Leu Asp Cys Leu Ser Val Gly Phe Asp Phe Pro
5 10 15

aac att ccc aga gct cct cgt tca tgc agg agg aag gtt cta aac aag 332
Asn Ile Pro Arg Ala Pro Arg Ser Cys Arg Arg Lys Val Leu Asn Lys
20 25 30

agg att gat cat gat gat gat aac act cag atc tgt gca att gac tta 380
Arg Ile Asp His Asp Asp Asp Asn Thr Gln Ile Cys Ala Ile Asp Leu
35 40 45

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Leu Ala Leu Ala Gly Lys Ile Leu Gln Glu Ser Glu Ser Ser Ser Ala
50 55 60 65

tct tct aat gca ttt gaa gaa att aag caa gag aaa gta gaa aat tgc 476
Ser Ser Asn Ala Phe Glu Glu Ile Lys Gln Glu Lys Val Glu Asn Cys
70 75 80

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cct Pro	act Thr	tat Tyr 100	gat Asp	atc Ile	tct Ser	act Thr	gag Glu 105	aag Lys	tgt Cys	gtg Val	gtg Val	aac Asn 110	agt Ser	tgt Cys	ttt Phe	572
tca Ser	ttt Phe 115	ccg Pro	gat Asp	agt Ser	gac Asp	ggc Gly 120	gtt Val	ttg Leu	gag Glu	cgg Arg	act Thr 125	ccg Pro	atg Met	tct Ser	gat Asp	620
tac Tyr 130	aag Lys	aag Lys	att Ile	cat His	ggg Gly 135	ttg Leu	atg Met	gat Asp	gta Val	ggg Gly 140	tgt Cys	gaa Glu	aac Asn	aag Lys	aat Asn 145	668
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cca Pro	tcc Ser 195	acc Thr	ttg Leu	gat Asp	atg Met	acc Thr 200	cct Pro	aat Asn	ggg Gly	tcc Ser	tat Tyr 205	gct Ala	aga Arg	cat His	ggg Gly	860
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cgc Arg	aaa Lys 275	aga Arg	aaa Lys	tca Ser	tgt Cys	tat Tyr 280	ggg Gly	tac Tyr	aac Asn	gca Ala	tgg Trp 285	cag Gln	cgt Arg	gag Glu	atc Ile	1100
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tta Leu 370	atg Met	cat His	ggg Gly	aag Lys	aag Lys 375	gtt Val	aga Arg	gat Asp	gaa Glu	agg Arg 380	aaa Lys	act Thr	ctg Leu	tcc Ser	cag Gln 385	1388
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aga Arg 450	aat Asn	att Ile	gtg Val	gac Asp	agt Ser 455	aac Asn	ctc Leu	gaa Glu	tta Leu	gtt Val 460	cca Pro	tat Tyr	cag Gln	ggg Gly	gac Asp 465	1628
ata Ile	tct Ser	gtt Val	gat Asp	gaa Glu 470	cct Pro	tca Ser	tca Ser	gat Asp	tca Ser 475	aaa Lys	gag Glu	ctt Leu	gtc Val	cca Pro 480	ctt Leu	1676
cca Pro	gag Glu	ttg Leu	gaa Glu 485	gtc Val	aag Lys	gcg Ala	ctt Leu	gcc Ala 490	ata Ile	gtt Val	ccg Pro	ttg Leu	aac Asn 495	cag Gln	aaa Lys	1724
cct Pro	aag Lys 500	cgt Arg	act Thr	gag Glu	cta Leu	gcc Ala	cag Gln 505	agg Arg	aga Arg	act Thr	agg Arg	aga Arg 510	ccc Pro	ttc Phe	tct Ser	1772
gtg Val	aca Thr 515	gag Glu	gta Val	gaa Glu	gct Ala	ctt Leu 520	gta Val	caa Gln	gca Ala	gtt Val 525	gag Glu	gaa Glu	ctc Leu	ggg Gly	act Thr	1820

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Ile	Arg	Arg	Ile	Arg	Lys	Ser	Met	Ser	Ser	Lys	Tyr	Trp	Lys	Gln	Val	
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Pro	Lys	Asp	Phe	Gly	Tyr	Ser	Arg	Ala	Asp	Val	Gly	Val	Lys	Thr	Leu	
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Tyr	Arg	Lys	Arg	Lys	Ser	Cys	Tyr	Gly	Tyr	Asn	Ala	Trp	Gln	Arg	Glu	
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 Ser Pro Met Leu Asp Ser Gly Ile Pro His Ala Asp Asp Val Ile Asp
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 Lys Pro Lys Arg Thr Glu Leu Ala Gln Arg Arg Thr Arg Arg Pro Phe
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 Ser Val Thr Glu Val Glu Ala Leu Val Gln Ala Val Glu Glu Leu Gly
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Gln	Asp	Lys	Ser	Gly	Lys	Asp	Cys	Gly	Pro	Asp	Lys	Ser	Leu	Ser	Val		
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aag aag cct cga ttg gtg aga ggt gca gct ggt tat aca cct gat att 899
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 225 230 235 240

gta gtg ggt cac cca ata cta gaa tca ggc ttg aac act tct tac cat 947
 Val Val Gly His Pro Ile Leu Glu Ser Gly Leu Asn Thr Ser Tyr His
 245 250 255

cag tca gac cat gtc ctc gcc ttt gac cag cca tct aca tca ctg ctt 995
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 260 265 270

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Val Met Gly Val Gln Gly Leu Thr Ile Tyr His Val Lys Ser His Leu
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Gln Lys Tyr Arg Leu Ala Lys Tyr Leu Pro Asp Ser Ser Ser Glu Gly
 65 70 75 80

Lys Lys Thr Asp Lys Lys Glu Ser Gly Asp Met Leu Ser Gly Leu Asp
 85 90 95

Gly Ser Ser Gly Met Gln Ile Thr Glu Ala Leu Lys Leu Gln Met Glu
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Val Gln Lys Arg Leu His Glu Gln Leu Glu Val Gln Arg Gln Leu Gln
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Leu Arg Ile Glu Ala Gln Gly Lys Tyr Leu Lys Lys Ile Ile Glu Glu
 130 135 140

Gln Gln Arg Leu Ser Gly Val Leu Gly Glu Pro Ser Ala Pro Val Thr
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Gly Asp Ser Asp Pro Ala Thr Pro Ala Pro Thr Ser Glu Ser Pro Leu
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Gln Asp Lys Ser Gly Lys Asp Cys Gly Pro Asp Lys Ser Leu Ser Val
 180 185 190

Asp Glu Ser Leu Ser Ser Tyr Arg Glu Pro Leu Thr Pro Asp Ser Gly
 195 200 205

Cys Asn Ile Gly Ser Pro Asp Glu Ser Thr Gly Glu Glu Arg Leu Ser
 210 215 220

Lys Lys Pro Arg Leu Val Arg Gly Ala Ala Gly Tyr Thr Pro Asp Ile
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Val Val Gly His Pro Ile Leu Glu Ser Gly Leu Asn Thr Ser Tyr His
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 may be A, T, C, G, other or unknown

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 Met Tyr

tcg gcg att cgg tct tcg ctt cct cta gat ggc agc ttg gga gac tac 165
 Ser Ala Ile Arg Ser Ser Leu Pro Leu Asp Gly Ser Leu Gly Asp Tyr
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tct gac gga acc aat ctt ccc atc gac gct tgt ctg gtc cta acc act 213
 Ser Asp Gly Thr Asn Leu Pro Ile Asp Ala Cys Leu Val Leu Thr Thr
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gac ccc aag cct cgc ctt cgt tgg acc tct gag ctc cat gaa aga ttc 261
 Asp Pro Lys Pro Arg Leu Arg Trp Thr Ser Glu Leu His Glu Arg Phe
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gtt gac gcc gtc act cag ctc ggc gga ccc gac aaa gca acg cct aaa 309
 Val Asp Ala Val Thr Gln Leu Gly Gly Pro Asp Lys Ala Thr Pro Lys
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act ata atg aga aca atg gga gtg aag ggt ctc act ctt tac cat ctc 357
 Thr Ile Met Arg Thr Met Gly Val Lys Gly Leu Thr Leu Tyr His Leu
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aaa tct cat ctt cag aaa ttc cgc ttg ggg agg caa tct tgt aaa gaa 405
 Lys Ser His Leu Gln Lys Phe Arg Leu Gly Arg Gln Ser Cys Lys Glu
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tca att gac aac tct aag gat gtt tct tgt gtt gcg gag agt cag gac 453
 Ser Ile Asp Asn Ser Lys Asp Val Ser Cys Val Ala Glu Ser Gln Asp
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 Thr Gly Ser Ser Ser Thr Ser Ser Leu Arg Leu Ala Ala Gln Glu Gln
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 Asn Glu Ser Tyr Gln Val Thr Glu Ala Leu Arg Ala Gln Met Glu Val
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 Gln Arg Arg Leu His Glu Gln Leu Glu Val Gln Arg Arg Leu Gln Leu
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tgc aag gct ata gag gag caa gct gtt gca ttt gct ggg tta gag gca 693
 Cys Lys Ala Ile Glu Glu Gln Ala Val Ala Phe Ala Gly Leu Glu Ala
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gct aga gaa gag ctt tca gag cta gcc ata aag gcc tcc atc acc aat 741
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 195 200 205 210

ggg tgc caa gga aca aca agc acc ttc gac aca acc aaa atg atg att 789
 Gly Cys Gln Gly Thr Thr Ser Thr Phe Asp Thr Thr Lys Met Met Ile
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cca tcc tta tcc gag ctt gca gta gca ata gag cac aag aac aac tgt 837
 Pro Ser Leu Ser Glu Leu Ala Val Ala Ile Glu His Lys Asn Asn Cys
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 Ser Ala Glu Ser Ser Leu Thr Ser Ser Thr Val Gly Ser Pro Val Ser
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 Ala Ala Leu Met Lys Lys Arg Gln Arg Gly Val Phe Gly Asn Gly Asp
 260 265 270

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 Ser Val Val Val Gly His Asp Ala Gly Trp Val Met Pro Ser Ser Ser
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att gga tgaagttagc aagagagaga gagagagcga gaccagattt tagcttattt 1037
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Asp Tyr Ser Asp Gly Thr Asn Leu Pro Ile Asp Ala Cys Leu Val Leu
 20 25 30

Thr Thr Asp Pro Lys Pro Arg Leu Arg Trp Thr Ser Glu Leu His Glu
 35 40 45

Arg Phe Val Asp Ala Val Thr Gln Leu Gly Gly Pro Asp Lys Ala Thr
 50 55 60

Pro Lys Thr Ile Met Arg Thr Met Gly Val Lys Gly Leu Thr Leu Tyr
 65 70 75 80

His Leu Lys Ser His Leu Gln Lys Phe Arg Leu Gly Arg Gln Ser Cys
 85 90 95

Lys Glu Ser Ile Asp Asn Ser Lys Asp Val Ser Cys Val Ala Glu Ser
 100 105 110

Gln Asp Thr Gly Ser Ser Ser Thr Ser Ser Leu Arg Leu Ala Ala Gln
 115 120 125

Glu Gln Asn Glu Ser Tyr Gln Val Thr Glu Ala Leu Arg Ala Gln Met
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 Glu Val Gln Arg Arg Leu His Glu Gln Leu Glu Val Gln Arg Arg Leu
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 Gln Leu Arg Ile Glu Ala Gln Gly Lys Tyr Leu Gln Ser Ile Leu Glu
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 Lys Ala Cys Lys Ala Ile Glu Glu Gln Ala Val Ala Phe Ala Gly Leu
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 Glu Ala Ala Arg Glu Glu Leu Ser Glu Leu Ala Ile Lys Ala Ser Ile
 195 200 205
 Thr Asn Gly Cys Gln Gly Thr Thr Ser Thr Phe Asp Thr Thr Lys Met
 210 215 220
 Met Ile Pro Ser Leu Ser Glu Leu Ala Val Ala Ile Glu His Lys Asn
 225 230 235 240
 Asn Cys Ser Ala Glu Ser Ser Leu Thr Ser Ser Thr Val Gly Ser Pro
 245 250 255
 Val Ser Ala Ala Leu Met Lys Lys Arg Gln Arg Gly Val Phe Gly Asn
 260 265 270
 Gly Asp Ser Val Val Val Gly His Asp Ala Gly Trp Val Met Pro Ser
 275 280 285
 Ser Ser Ile Gly
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